

CAB89082.1	AJ277534	Asparagus officinalis S6 ribosomal protein kinase. pk1. putative.
AAB93862.1	U89681	Lycopersicon esculentum protein kinase. LePK4. contains catalytic domain.
BAA92972.1	AP001551	Oryza sativa ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).
BAB12687.1	AP002746	Oryza sativa putative protein kinase. P0671B11.2. contains ESTs C22394(C30013),C22393(C30013).
		SEQ ID NO: 508
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
CAA74662.1	Y14286	Brassica oleracea SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA74661.1	Y14285	Brassica oleracea SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
CAA73133.1	Y12530	Brassica oleracea serine /threonine kinase. ARLK.
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
AAA33008.1	M97667	Brassica napus serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus ser /thr kinase. S-locus receptor kinase. srk.
CAA79355.1	Z18921	Brassica oleracea S-receptor kinase-like protein.
CAB41878.1	Y18259	Brassica oleracea SRK5 protein. SRK5. receptor-like kinase.
AAA33000.1	M76647	Brassica oleracea receptor protein kinase. SKR6.
BAA92837.1	AB032474	Brassica oleracea S60 S-locus receptor kinase. SRK60.
BAA21132.1	D88193	Brassica rapa S-receptor kinase. SRK9 (B.c.).
BAA06285.1	D30049	Brassica rapa S-receptor kinase SRK9.
AAA62232.1	U00443	Brassica napus S-receptor kinase. protein contains an immunoglobulin-like domain.
BAA92836.1	AB032473	Brassica oleracea S18 S-locus receptor kinase. SRK18.

BAB21001.1	AB054061	Brassica rapa S locus receptor kinase. SRK22.
BAA07576.1	D38563	Brassica rapa receptor protein kinase SRK8.
BAA07577.2	D38564	Brassica rapa receptor protein kinase SRK12.
CAA73134.1	Y12531	Brassica oleracea serine/threonine kinase. BRLK.
AAB93834.1	U82481	Zea mays KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
CAB41879.1	Y18260	Brassica oleracea SRK15 protein. SRK15. receptor-like kinase.
AAD52097.1	AF088885	Nicotiana tabacum receptor-like kinase CHRK1. Chrk1.
AAD21872.1	AF078082	Phaseolus vulgaris receptor-like protein kinase homolog RK20-1.
BAB18292.1	AP002860	Oryza sativa putative receptor-like protein kinase. P0409B08.19.
AAK02023.1	AC074283	Oryza sativa Putative protein kinase-like. OSJNBa0087H07.5.
CAA79324.1	Z18884	Brassica oleracea S-receptor kinase related protein.
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
CAB51836.1	AJ243961	Oryza sativa Putitive Ser/Thr protein kinase. 11332.7.
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
BAA94509.1	AB041503	Populus nigra protein kinase 1. PnPK1.
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
BAA94510.1	AB041504	Populus nigra protein kinase 2. PnPK2.
BAA92953.1	AP001551	Oryza sativa Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).

BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
AAG16628.1	AY007545	Brassica napus protein serine/threonine kinase BNK1.
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
SEQ ID NO: 510		
AAG30254.1	AF307333	Hordeum vulgare putative nematode-resistance protein. Hs1. similar to Beta procumbens Hs1pro protein.
AAB48305.1	U79733	Beta procumbens nematode resistance. Hs1pro-1.
SEQ ID NO: 513		
BAA14144.1	D90116	Armoracia rusticana peroxidase isozyme.
BAA14143.1	D90115	Armoracia rusticana peroxidase isozyme.
BAA11853.1	D83225	Populus nigra peroxidase.
CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA11852.1	D83224	Populus nigra peroxidase.
BAA07241.1	D38051	Populus kitakamiensis peroxidase. prxA4a.
BAA06335.1	D30653	Populus kitakamiensis peroxidase.
AAB47602.1	L07554	Linum usitatissimum peroxidase. FLXPER1.
AAC98519.1	AF007211	Glycine max peroxidase precursor. GMIPER1. pathogen-induced.
AAD37427.1	AF149277	Phaseolus vulgaris peroxidase 1 precursor. FBP1. secretory peroxidase.
BAA06334.1	D30652	Populus kitakamiensis peroxidase.
AAB97734.1	AF014502	Glycine max seed coat peroxidase precursor. Ep. H2O2 oxidoreductase; class III plant peroxidase.

CAB94692.1	AJ242742	Ipomoea batatas Removal of H ₂ O ₂ , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
CAA62227.1	X90694	Medicago sativa peroxidase1C. prx1C.
CAA62226.1	X90693	Medicago sativa peroxidase1B. prx1B.
AAD37430.1	AF149280	Phaseolus vulgaris peroxidase 5 precursor. FBP5. secretory peroxidase.
CAA62225.1	X90692	Medicago sativa peroxidase1A. prx1A.
AAB41811.1	L36157	Medicago sativa peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.
AAB41810.1	L36156	Medicago sativa peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
BAA01877.1	D11102	Populus kitakamiensis peroxidase. prxA1.
CAB67121.1	Y19023	Lycopersicon esculentum peroxidase. cevi-1.
CAA50597.1	X71593	Lycopersicon esculentum peroxidase. CEVI-1.
BAA01992.1	D11396	Nicotiana tabacum 'peroxidase'.
AAA34108.1	J02979	Nicotiana tabacum lignin-forming peroxidase precursor (EC 1.11.1.7).
AAA33127.1	M91373	Cucumis sativus peroxidase. pre-peroxidase. putative.
BAA92500.1	AP001383	Oryza sativa ESTs D39300(R3292),AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).
CAB65334.1	AJ250121	Picea abies peroxidase. SPI2 protein. spi2.
CAA40796.1	X57564	Armoracia rusticana peroxidase. peroxidase precursor.
AAB06183.1	M37636	Arachis hypogaea cationic peroxidase. PNC1.
CAA76680.1	Y17192	Cucurbita pepo peroxidase. aprx. type III peroxidase.
AAA33129.1	M91372	Cucumis sativus peroxidase. pre-peroxidase.

CAA71492.1	Y10466	Spinacia oleracea peroxidase. prxr5.
AAF63027.1	AF244924	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
AAD43561.1	AF155124	Gossypium hirsutum bacterial-induced peroxidase precursor. Perx_Goshiko.
AAF63026.1	AF244923	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx14 precursor. type III peroxidase.
AAA33121.1	M32742	Cucumis sativus peroxidase (CuPer2).
BAA92422.1	AP001366	Oryza sativa ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to A.thaliana mRNA for peroxidase ATP18a. (X98804).
BAA92497.1	AP001383	Oryza sativa ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to peroxidase ATP18a. (X98804).
BAA77389.1	AB024439	Scutellaria baicalensis peroxidase 3.
BAA08499.1	D49551	Oryza sativa peroxidase. poxN.
AAB19129.1	U41657	Glycine max seed coat peroxidase isozyme. SPOD4.1. H2O2 oxidoreductase.
BAA03373.1	D14482	Oryza sativa putative peroxidase.
AAB02554.1	L37790	Stylosanthes humilis cationic peroxidase.
SEQ ID NO: 515		
AAB88134.1	AF034618	Spinacia oleracea cytosolic heat shock 70 protein. HSC70-1.
AAF34134.1	AF161180	Malus x domestica high molecular weight heat shock protein. Hsp2.
AAB99745.1	AF005993	Triticum aestivum HSP70. TaHSP70d. 70 kDa heat shock protein, molecular chaperone.
AAA62325.1	L32165	Hordeum vulgare Molecular chaperone. HSP70. Heat-shock protein HSP70; The predicted amino acid sequence is highly homologous (more than 80% identity) to other plant heat-shock proteins (HSP70s) in the database; however the C terminus is quite unique.; putative.
AAA21808.1	L23551	Spinacia oleracea molecular chaperone. ER-lumenal protein. HSC70.
AAA34139.1	L08830	Lycopersicon esculentum molecular chaperon (precursor). glucose-regulated protein 78. BiP/grp78. an endoplasmic reticulum residing heat shock protein 70 family member; precursor peptide.

AAB86942.1	AF031241	Glycine max endoplasmic reticulum transport protein; molecular chaperone; roles in protein folding, assembly, and transport. endoplasmic reticulum HSC70-cognate binding protein precursor. BiP. BiP; similar to HSC70 and GRP78.
AAK21920.1	AF338252	Glycine max molecular chaperone. BiP-isoform D. BiPD. ER-luminal HSP70; binding protein GRP78.
AAB91473.1	AF035458	Spinacia oleracea heat shock 70 protein. HSC70-11. mitochondrial protein.
AAB96660.1	AF039084	Spinacia oleracea heat shock 70 protein. HSC70-11. molecular chaperone.
AAB91472.1	AF035457	Spinacia oleracea heat shock 70 protein. HSC70-10. mitochondrial protein.
		SEQ ID NO: 516
CAA06927.1	AJ006233	Nicotiana tabacum putative thaumatin-like protein precursor.
AAF06346.1	AF195653	Vitis vinifera SCUTL1. thaumatin-like protein.
BAA28872.1	AB006009	Pyrus pyrifolia thaumatin-like protein precursor. PsTL1.
CAC10270.1	AJ243427	Malus x domestica thaumatin-like protein. tl. allergen, pathogenesis-related.
AAC36740.1	AF090143	Malus x domestica thaumatin-like protein precursor Mdtl1. MDTL1. pathogenesis-related.
CAB62167.1	AJ242828	Castanea sativa antifungal. thaumatin-like protein. tl1.
AAB38064.1	U32440	Prunus avium thaumatin-like protein precursor.
BAA74546.2	AB000834	Nicotiana tabacum thaumatin-like protein SE39b.
AAF06347.1	AF195654	Vitis vinifera SCUTL2. thaumatin-like protein.
CAC09477.1	AL442113	Oryza sativa thaumatin-like protein. H0806H05.10.
AAB95118.1	U71244	Brassica rapa pathogenesis-related group 5 protein. BFTP. thaumatin-like protein; PR-5.
CAA10492.1	AJ131731	Pseudotsuga menziesii Thaumatin-like protein. 5A1A.16.
BAA95017.1	AB031870	Cestrum elegans thaumatin-like protein. CETLP.
BAA95165.1	AB029918	Nicotiana tabacum pistil transmitting tissue specific thaumatin (SE39b)-like protein. SE39b.
AAB61590.1	AF003007	Vitis vinifera VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.

AAD55090.1 AF178653 Vitis riparia
thaumatin. osmotin; pathogenesis-related protein.

CAB85637.1 AJ237999 Vitis vinifera
putative thaumatin-like protein. Tl1. alternative name grip 51.

AAF82264.1 AF227324 Vitis vinifera
thaumatin-like protein.

AAB02259.1 U57787 Avena sativa
permatin precursor. thaumatin-like protein.

AAB53368.1 U77657 Oryza sativa
pathogenesis-related thaumatin-like protein.

CAA09228.1 AJ010501 Cicer arietinum
thaumatin-like protein PR-5b.

CAA33293.1 X15224 Nicotiana tabacum
thaumatin-like protein. E22.

CAA33292.1 X15223 Nicotiana tabacum
thaumatin-like protein. E2.

SEQ ID NO: 517

CAA71801.1 Y10848 Brassica juncea
gamma-glutamylcysteine synthetase. gsh1.

AAB71230.1 AF017983 Lycopersicon esculentum
gamma-glutamylcysteine synthetase. GSH1.

AAC82334.1 AF041340 Medicago truncatula
gamma-glutamylcysteine synthetase. putative plastid protein.

AAF22137.1 AF128455 Pisum sativum
gamma-glutamylcysteine synthetase precursor. gsh1. putative plastid protein.

AAF22136.1 AF128454 Phaseolus vulgaris
gamma-glutamylcysteine synthetase precursor. gsh1. putative plastid protein.

CAA06613.1 AJ005587 Brassica juncea
gamma-glutamylcysteine synthetase.

AAG13459.1 AF128453 Glycine max
gamma-glutamylcysteine synthetase precursor. gsh1.

CAA64808.1 X95563 Brassica juncea
gamma-glutamylcysteine synthetase. gsh1.

SEQ ID NO: 518

AAA75414.1 L28005 Glycine max
TGACG-motif-binding protein. STGA1.

AAB31250.2 S73827 Solanum tuberosum
mas-binding factor MBF3. transcription factor TGA1a homolog; This sequence comes from Fig. 4.

AAB31249.1 S73826 Solanum tuberosum
mas-binding factor MBF2. mas-binding factor MBF2. transcription factor TGA1a homolog; This sequence comes from Fig. 4.

CAA34468.1	X16449	Nicotiana sp.
TGA1a protein (AA 1-359).		
AAA34091.1	M62855	Nicotiana tabacum
ASF-1/G13. leucine-zipper DNA-binding protein.		
AAB31251.2	S73828	Solanum tuberosum
mas-binding factor MBF1. transcription factor TGA1a homolog; This sequence comes from Fig. 4.		
CAA48904.1	X69152	Zea mays
ocs-element binding factor 3.2. OBF3.2.		
CAA48905.1	X69153	Zea mays
ocs-element binding factor 3.1. OBF3.1.		
AAC24123.1	AF067187	Cichorium intybus
cAMP responsive element binding protein. bZIP transcription factor; CREB.		
AAC24122.1	AF067186	Cichorium intybus
cAMP responsive element binding protein. CREB1.		
AAC49760.1	AF001454	Helianthus annuus
Dc3 promoter-binding factor-2. DPBF-2.		
SEQ ID NO: 521		
CAA10608.1	AJ132228	Ricinus communis
amino acid carrier. aap3.		
CAA07563.1	AJ007574	Ricinus communis
amino acid carrier. aap1.		
CAA70778.1	Y09591	Vicia faba
amino acid transporter.		
AAD16014.1	AF080543	Nepenthes alata
amino acid transporter. AAP2.		
CAA70969.1	Y09826	Solanum tuberosum
amino acid transporter. AAP2. transmembrane protein.		
AAD16015.1	AF080544	Nepenthes alata
amino acid transporter. AAP3.		
CAA70968.1	Y09825	Solanum tuberosum
amino acid transporter. AAP1. transmembrane protein.		
CAA92992.1	Z68759	Ricinus communis
amino acid carrier.		
AAD16013.1	AF080542	Nepenthes alata
amino acid transporter. AAP1.		
AAF15945.1	AF061435	Vicia faba
amino acid transporter b. AAPB.		
CAA72006.1	Y11121	Ricinus communis
amino acid carrier.		
AAF15944.1	AF061434	Vicia faba
amino acid transporter a. AAPA.		

AAF15946.1 AF061436	<i>Vicia faba</i>
amino acid transporter c.	AAPC.
AAB48944.1 U31932	<i>Nicotiana sylvestris</i>
amino acid permease 1.	NSAAP1. amino acid transporter; Method: conceptual translation supplied by author.
AAB96830.1 U64823	<i>Nicotiana sylvestris</i>
amino acid transporter.	amino acid permease. nsaap1.
BAA93437.1 AB022783	<i>Oryza sativa</i>
amino acid permease.	OsproT.
AAD25162.1 AF014810	<i>Lycopersicon esculentum</i>
proline transporter 3.	LeProT3.
AAD25161.1 AF014809	<i>Lycopersicon esculentum</i>
proline transporter 2.	LeProT2.
AAD25160.1 AF014808	<i>Lycopersicon esculentum</i>
proline transporter 1.	LeProT1.
AAF76897.1 AF274032	<i>Atriplex hortensis</i>
proline/glycine betaine transporter.	
CAB42599.1 AJ238635	<i>Chlorella protothecoides</i>
amino acid carrier.	dee4.

SEQ ID NO: 526

BAA03763.1 D16247	<i>Nicotiana sylvestris</i>
RNA helicase like protein DB10.	
AAD46404.1 AF096248	<i>Lycopersicon esculentum</i>
ethylene-responsive RNA helicase.	ER68. putative DEAD box/RNA helicase.
AAF75791.1 AF271892	<i>Pisum sativum</i>
DEAD box protein P68.	P68. RNA helicase.
AAF40306.1 AF156667	<i>Vigna radiata</i>
RNA helicase.	VRH1.
CAA68193.1 X99937	<i>Spinacia oleracea</i>
RNA helicase.	prh75. DEAD-box protein; homologous to X99938.
AAG13612.1 AC078840	<i>Oryza sativa</i>
putative RNA helicase.	OSJNBb0073N24.12.
AAG34876.1 AF261021	<i>Nicotiana tabacum</i>
putative chloroplast RNA helicase VDL isoform 1.	VDL. alternatively spliced.
AAG34873.1 AF261020	<i>Nicotiana tabacum</i>
putative chloroplast RNA helicase VDL isoform 1.	VDL. essential for chloroplast development; may be involved in post-transcriptional regulation.
AAG34879.1 AF261024	<i>Nicotiana tabacum</i>
putative chloroplast RNA helicase VDL' isoform 1.	VDL'. alternatively spliced.
AAD20980.1 AF079782	<i>Zea mays</i>
ATPase and RNA helicase.	translation initiation factor 4A2. tif4A2.
AAG34882.1 AF261027	<i>Nicotiana tabacum</i>
putative chloroplast RNA helicase VDL' isoform 4.	VDL'. alternatively spliced.

BAA95705.1 AB042644 *Oryza sativa*
DEAD box RNA helicase OsPL10b. OsPL10b.

BAA95704.1 AB042643 *Oryza sativa*
DEAD box RNA helicase OsPL10a. OsPL10a.

AAG34883.1 AF261028 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL' isoform 5. VDL'. alternatively spliced.

AAG38493.1 AF261032 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL' isoform 1. VDL'. alternatively spliced.

AAG34884.1 AF261029 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL' isoform 6. VDL'. alternatively spliced.

AAG38496.1 AF261032 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL' isoform 4. VDL'. alternatively spliced.

AAG38497.1 AF261032 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL' isoform 5. VDL'. alternatively spliced.

AAG38498.1 AF261032 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL' isoform 6. VDL'. alternatively spliced.

AAG38500.1 AF261032 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL' isoform 8. VDL'. alternatively spliced.

AAG34886.1 AF261031 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL' isoform 8. VDL'. alternatively spliced.

AAG48833.1 AC084218 *Oryza sativa*
similar to *Arabidopsis thaliana* DNA helicase (AJ404475).

SEQ ID NO: 528

CAA65536.1 X96761 *Sporobolus stapfianus*
sulphate transporter protein.

AAK27688.1 AF347614 *Lycopersicon esculentum*
sulfate transporter 2. ST2.

AAK27687.1 AF347613 *Lycopersicon esculentum*
sulfate transporter 1. ST1.

CAA57711.1 X82256 *Stylosanthes hamata*
high affinity sulphate transporter. SHST2.

AAG41419.1 AF309643 *Solanum tuberosum*
high affinity sulfate transporter type 1. ST1.

CAA57710.1 X82255 *Stylosanthes hamata*
high affinity sulphate transporter. SHST1.

AAK35215.1 AF355602 *Zea mays*
sulfate transporter ST1.

CAA65291.1 X96431 *Hordeum vulgare*
high affinity sulphate transporter. HVST1.

AAA97952.1 U52867 *Hordeum vulgare*
high affinity sulfate transporter HVST1.

CAB42985.1 AJ238244 *Aegilops tauschii*
putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st1.

CAB42986.1 AJ238245 *Aegilops tauschii*
putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st2.

CAA57831.1 X82454 *Stylosanthes hamata*
low affinity sulphate transporter. SHST3.

SEQ ID NO: 531

AAK00436.1 AC060755 *Oryza sativa*
putative zinc finger protein. OSJNBa0003O19.23.

BAA85438.1 AP000616 *Oryza sativa*
similar to RING-H2 finger protein RHA1a (AF078683).

AAG43550.1 AF211532 *Nicotiana tabacum*
Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.

BAA90357.1 AP001080 *Oryza sativa*
EST AU070319(S10788) corresponds to a region of the predicted gene. Similar to RING-H2 finger protein RHA2b (AC006200).

SEQ ID NO: 532

BAA81751.1 AB017517 *Marchantia polymorpha*
calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.

BAA13232.1 D87042 *Zea mays*
Calcium-dependent protein kinase.

BAA81749.1 AB017515 *Marchantia polymorpha*
calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.

BAA81750.1 AB017516 *Marchantia polymorpha*
calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.

BAA85396.1 AP000615 *Oryza sativa*
ESTs C22369(C12239),C22370(C12239), AU057852(S21844),AU057853(S21844)
correspond to a region of the predicted gene.; similar to calcium dependent protein kinase.
(AF048691).

CAA57156.1 X81393 *Oryza sativa*
calcium-dependent protein kinase. OSCPKII.

AAC05270.1 AF048691 *Oryza sativa*
calcium dependent protein kinase. CDPK12.

AAB49984.1 U90262 *Cucurbita pepo*
calcium-dependent calmodulin-independent protein kinase CDPK. cpCPK1. serine/threonine
protein kinase that is activated by direct binding of calcium.

AAB70706.1 U82087 *Tortula ruralis*
calmodulin-like domain protein kinase. TrCPK1.

AAG46110.1 AC073166 *Oryza sativa*
calcium-dependent protein kinase. OSJNBb0064P21.2.

BAA02698.1 D13436 *Oryza sativa*
calcium-dependent protein kinase. spk.

BAA81748.1	AB017515	<i>Marchantia polymorpha</i> calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
CAA07481.1	AJ007366	<i>Zea mays</i> calcium-dependent protein kinase.
AAB80692.1	U69173	<i>Glycine max</i> calmodulin-like domain protein kinase isoenzyme beta. CDPK beta.
AAC49405.1	U08140	<i>Vigna radiata</i> calcium dependent protein kinase. CDPK.
BAA12338.1	D84408	<i>Zea mays</i> calcium dependent protein kinase. ZmCDPK1.
AAA33443.1	L15390	<i>Zea mays</i> calcium-dependent protein kinase. CDPK.
CAA57157.1	X81394	<i>Oryza sativa</i> calcium-dependent protein kinase. OSCPK2.
BAB21081.1	AP002819	<i>Oryza sativa</i> putative calcium-dependent protein kinase. P0501G01.10.
BAA12715.1	D85039	<i>Zea mays</i> calcium-dependent protein kinase.
CAA65500.1	X96723	<i>Medicago sativa</i> protein kinase. CDPK.
AAC25423.1	AF072908	<i>Nicotiana tabacum</i> calcium-dependent protein kinase. CDPK1.
AAA69507.1	U28376	<i>Zea mays</i> calcium-dependent protein kinase. MZECDPK2.
BAA13440.1	D87707	<i>Ipomoea batatas</i> calcium dependent protein kinase. CDPK.
AAD28192.2	AF115406	<i>Solanum tuberosum</i> calcium-dependent protein kinase. CDPK; catalytic domain.
AAB80693.1	U69174	<i>Glycine max</i> calmodulin-like domain protein kinase isoenzyme gamma. CDPK gamma.
AAA61682.1	L27484	<i>Zea mays</i> calcium-dependent protein kinase. CDPK.
AAD17800.1	AF090835	<i>Mesembryanthemum crystallinum</i> Ca2+-dependent protein kinase. CPK1. serine/threonine protein kinase.
CAA39936.1	X56599	<i>Daucus carota</i> calcium- dependent protein kinase. DcPK431.
AAK26164.1	AY027885	<i>Cucumis sativus</i> calcium-dependent calmodulin-independent protein kinase 5. CDPK5. CsCDPK5.
AAB88537.1	AF035944	<i>Fragaria x ananassa</i> calcium-dependent protein kinase. MAX17.
AAF21062.1	AF216527	<i>Dunaliella tertiolecta</i> calcium-dependent protein kinase. CPK1; CDPK.

CAA89202.1	Z49233	Chlamydomonas eugametos calcium-stimulated protein kinase.
AAC32116.1	AF051211	Picea mariana probable calcium dependent protein kinase. Sb15. similar to Vigna radiata calcium dependent protein kinase encoded by U08140.
AAF23900.1	AF194413	Oryza sativa calcium-dependent protein kinase. CDPK1. OsCDPK1.
AAF23901.2	AF194414	Oryza sativa calcium-dependent protein kinase. CDPK5. OsCDPK5.
CAB46228.1	Y18055	Arachis hypogaea calcium dependent protein kinase. CDPK.
AAC78558.1	AF030879	Solanum tuberosum protein kinase CPK1.
CAA58750.1	X83869	Daucus carota CDPK-related protein kinase. CRK (or PK421).
AAB47181.1	S82324	Zea mays /gene="calcium/calmodulin-dependent protein kinase. This sequence comes from Fig. 1.
BAA12691.1	D84507	Zea mays CDPK-related protein kinase. Does not require calcium for its activity (by similarity).
BAA22410.1	D38452	Zea mays calcium-dependent protein kinase-related kinase.
BAA12692.1	D84508	Zea mays CDPK-related protein kinase. Does not require calcium for its activity.
AAG01179.1	AF289237	Zea mays calcium/calmodulin dependent protein kinase MCK2. MCK2.
AAC24961.1	AF009337	Tradescantia virginiana CDPK-related protein kinase. CRK1.
BAA90814.1	AP001168	Oryza sativa ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.; Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).
AAC49008.1	U24188	Lilium longiflorum calcium/calmodulin-dependent phosphorylation activity. calcium/calmodulin-dependent protein kinase. CCaMK. serine/threonine kinase; binds to calcium and calmodulin.
AAF19402.1	AF203480	Lycopersicon esculentum phosphoenolpyruvate carboxylase kinase, protein kinase; member of Ca2+/CaM kinase family; lacks the autoinhibitory region and EF hands.

SEQ ID NO: 535

AAK19619.1	AF336286	Gossypium hirsutum GHMYB9. ghmyb9. similar to myb.
CAA64614.1	X95296	Lycopersicon esculentum transcription factor. THM27. myb-related.
CAA50224.1	X70879	Hordeum vulgare MybHv1. myb1.

CAA50222.1	X70877	Hordeum vulgare MybHv1. myb1.
AAA33067.1	L04497	Gossypium hirsutum MYB A; putative.
CAA50221.1	X70876	Hordeum vulgare MybHv5. myb2.
BAA23337.1	D88617	Oryza sativa transfactor. OSMYB1. Osmyb1.
BAA23338.1	D88618	Oryza sativa transfactor. OSMYB2. Osmyb2.
AAC04720.1	AF034134	Gossypium hirsutum putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-O. similar to MYB A encoded by GenBank Accession Number L04497.
CAA72218.1	Y11415	Oryza sativa myb.
CAA50225.1	X70880	Hordeum vulgare MybHv5. myb2.
AAA82943.1	U39448	Picea mariana MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.
CAA78386.1	Z13996	Petunia x hybrida DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
BAA81732.1	AB029161	Glycine max GmMYB29A2.
AAK19616.1	AF336283	Gossypium hirsutum GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.
AAK19611.1	AF336278	Gossypium hirsutum BNLGH1233. bnlghi6233. similar to myb.
AAK19617.1	AF336284	Gossypium hirsutum GHMYB36. ghmyb36. similar to myb.
BAA93038.1	AP001552	Oryza sativa EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
AAK19615.1	AF336282	Gossypium hirsutum GHMYB10. ghmyb10. similar to myb.
BAB39987.1	AP003020	Oryza sativa putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
BAB39972.1	AP003018	Oryza sativa putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).

CAB43399.1	AJ006292	Antirrhinum majus Myb-related transcription factor mixta-like 1. mybml1.
CAA72185.1	Y11350	Oryza sativa myb factor. myb.
AAF22256.1	AF161711	Pimpinella brachycarpa myb-related transcription factor.
AAG13574.1	AC037425	Oryza sativa myb factor. OSJNBa0055P24.4.
BAA81731.1	AB029160	Glycine max GmMYB29A1.
BAA81730.1	AB029159	Glycine max GmMYB29A1.
CAA72186.1	Y11351	Oryza sativa myb factor. myb.
CAA67600.1	X99210	Lycopersicon esculentum myb-related transcription factor. THM16.
CAA75509.1	Y15219	Oryza sativa subsp. indica transcriptional activator. C1.
AAC04718.1	AF034132	Gossypium hirsutum putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-J. similar to MYB A encoded by GenBank Accession Number L04497.
CAA78387.1	Z13997	Petunia x hybrida DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
BAA81736.1	AB029165	Glycine max GmMYB29B2.
AAK19618.1	AF336285	Gossypium hirsutum GHMYB38. ghmyb38. similar to myb.
CAA72217.1	Y11414	Oryza sativa myb.
AAC49394.1	U57002	Zea mays P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.
AAA33500.1	M73028	Zea mays myb-like transcription factor. P.
BAB20661.1	AP002871	Oryza sativa putative myb-related protein P. P0475H04.31.
AAG36774.1	AF210616	Zea mays P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.
BAA88222.1	AB028650	Nicotiana tabacum myb-related transcription factor LBM2. lbm2.
BAA81733.2	AB029162	Glycine max GmMYB29A2.

BAA23339.1 D88619 *Oryza sativa*
transfactor. OSMYB3. Osmyb3.

BAA88224.1 AB028652 *Nicotiana tabacum*
myb-related transcription factor LBM4. lbm4.

BAA88221.1 AB028649 *Nicotiana tabacum*
myb-related transcription factor LBM1. lbm1.

AAB41101.1 U72762 *Nicotiana tabacum*
transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.

SEQ ID NO: 536

CAA70968.1 Y09825 *Solanum tuberosum*
amino acid transporter. AAP1. transmembrane protein.

AAF15946.1 AF061436 *Vicia faba*
amino acid transporter c. AAPC.

CAA70969.1 Y09826 *Solanum tuberosum*
amino acid transporter. AAP2. transmembrane protein.

AAB96830.1 U64823 *Nicotiana sylvestris*
amino acid transporter. amino acid permease. nsaap1.

CAA07563.1 AJ007574 *Ricinus communis*
amino acid carrier. aap1.

AAB48944.1 U31932 *Nicotiana sylvestris*
amino acid permease 1. NSAAP1. amino acid transporter; Method: conceptual translation supplied by author.

AAD16015.1 AF080544 *Nepenthes alata*
amino acid transporter. AAP3.

CAA70778.1 Y09591 *Vicia faba*
amino acid transporter.

AAF15944.1 AF061434 *Vicia faba*
amino acid transporter a. AAPA.

AAF15945.1 AF061435 *Vicia faba*
amino acid transporter b. AAPB.

AAF76897.1 AF274032 *Atriplex hortensis*
proline/glycine betaine transporter.

AAD16014.1 AF080543 *Nepenthes alata*
amino acid transporter. AAP2.

AAD25161.1 AF014809 *Lycopersicon esculentum*
proline transporter 2. LeProT2.

CAA10608.1 AJ132228 *Ricinus communis*
amino acid carrier. aap3.

SEQ ID NO: 537

BAA89009.1 AB027455 *Petunia x hybrida*
anthocyanin 5-O-glucosyltransferase. PH1.

BAA36423.1	AB013598	<i>Verbena x hybrida</i> UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
BAA36421.1	AB013596	<i>Perilla frutescens</i> UDP-glucose:anthocysnin 5-O-glucosyltransferase. PF3R4.
BAB07962.1	AP002524	<i>Oryza sativa</i> putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
BAA36422.1	AB013597	<i>Perilla frutescens</i> UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.
BAA93039.1	AB033758	<i>Citrus unshiu</i> limonoid UDP-glucosyltransferase. LGTase.
AAF61647.1	AF190634	<i>Nicotiana tabacum</i> UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
AAF98390.1	AF287143	<i>Brassica napus</i> catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
AAK16175.1	AC079887	<i>Oryza sativa</i> putative glucosyltransferase. OSJNBa0040E01.15.
AAF17077.1	AF199453	<i>Sorghum bicolor</i> UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
AAK16172.1	AC079887	<i>Oryza sativa</i> putative glucosyltransferase. OSJNBa0040E01.14.
BAA83484.1	AB031274	<i>Scutellaria baicalensis</i> UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAK16181.1	AC079887	<i>Oryza sativa</i> putative glucosyltransferase. OSJNBa0040E01.16.
AAG25643.1	AF303396	<i>Phaseolus vulgaris</i> UDP-glucosyltransferase HRA25. putative; defense associated.
AAK16178.1	AC079887	<i>Oryza sativa</i> putative glucosyltransferase. OSJNBa0040E01.5..
AAD21086.1	AF127218	<i>Forsythia x intermedia</i> adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
BAA12737.1	D85186	<i>Gentiana triflora</i> UDP-glucose:flavonoid-3-glucosyltransferase.
AAK28303.1	AF346431	<i>Nicotiana tabacum</i> phenylpropanoid:glucosyltransferase 1. tog1. glucosyltransferase.
CAB56231.1	Y18871	<i>Dorotheanthus bellidiformis</i> betanidin-5-O-glucosyltransferase.
CAA54612.1	X77462	<i>Manihot esculenta</i> UTP-glucose glucosyltransferase. CGT5.

BAB41019.1	AB047092	<i>Vitis vinifera</i>
UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.		
BAB41020.1	AB047093	<i>Vitis vinifera</i>
UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.		
AAB36653.1	U32644	<i>Nicotiana tabacum</i>
immediate-early salicylate-induced glucosyltransferase. ISSa.		
BAB41025.1	AB047098	<i>Vitis vinifera</i>
UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.		
BAB41023.1	AB047096	<i>Vitis vinifera</i>
UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.		
BAB41022.1	AB047095	<i>Vitis vinifera</i>
UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.		
BAB41021.1	AB047094	<i>Vitis vinifera</i>
UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.		
BAA19659.1	AB002818	<i>Perilla frutescens</i>
flavonoid 3-O-glucosyltransferase. UDP glucose.		
BAB41026.1	AB047099	<i>Vitis vinifera</i>
UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.		
BAB41024.1	AB047097	<i>Vitis vinifera</i>
UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.		
AAK16180.1	AC079887	<i>Oryza sativa</i>
putative glucosyltransferase. OSJNBA0040E01.21.		
AAK28304.1	AF346432	<i>Nicotiana tabacum</i>
phenylpropanoid:glucosyltransferase 2. tog2. glucosyltransferase.		
AAB36652.1	U32643	<i>Nicotiana tabacum</i>
immediate-early salicylate-induced glucosyltransferase. IS10a.		
BAB41017.1	AB047090	<i>Vitis labrusca x Vitis vinifera</i>
UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.		
BAA89008.1	AB027454	<i>Petunia x hybrida</i>
anthocyanidin 3-O-glucosyltransferase. PGT8.		
CAA59450.1	X85138	<i>Lycopersicon esculentum</i>
tw1. homologous to glucosyltransferases.		
CAA54614.1	X77464	<i>Manihot esculenta</i>
UTP-glucose glucosyltransferase. CGT7.		
CAA54611.1	X77461	<i>Manihot esculenta</i>
UTP-glucose glucosyltransferase. CGT2.		
CAA54613.1	X77463	<i>Manihot esculenta</i>
UTP-glucose glucosyltransferase. CGT6.		
SEQ ID NO: 540		
AAK27688.1	AF347614	<i>Lycopersicon esculentum</i>
sulfate transporter 2. ST2.		

AAG41419.1	AF309643	<i>Solanum tuberosum</i> high affinity sulfate transporter type 1. ST1.
AAK27687.1	AF347613	<i>Lycopersicon esculentum</i> sulfate transporter 1. ST1.
AAA97952.1	U52867	<i>Hordeum vulgare</i> high affinity sulfate transporter HVST1.
CAA57711.1	X82256	<i>Stylosanthes hamata</i> high affinity sulphate transporter. SHST2.
CAA65291.1	X96431	<i>Hordeum vulgare</i> high affinity sulphate transporter. HVST1.
CAA57710.1	X82255	<i>Stylosanthes hamata</i> high affinity sulphate transporter. SHST1.
CAB42985.1	AJ238244	<i>Aegilops tauschii</i> putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st1.
AAK35215.1	AF355602	<i>Zea mays</i> sulfate transporter ST1.
CAB42986.1	AJ238245	<i>Aegilops tauschii</i> putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st2.
CAA65536.1	X96761	<i>Sporobolus stapfianus</i> sulphate transporter protein.
CAA57831.1	X82454	<i>Stylosanthes hamata</i> low affinity sulphate transporter. SHST3.
CAA11413.1	AJ223495	<i>Brassica juncea</i> sulfate permease. sp1.
AAB94543.1	AF016306	<i>Zea mays</i> sulfate permease.
SEQ ID NO: 541		
AAF36491.1	AF129479	<i>Hordeum vulgare</i> HAK2. HAK2. similar to <i>Hordeum vulgare</i> K ⁺ transporter HAK1.
BAB32443.1	AB055630	<i>Phragmites australis</i> high-affinity potassium transporter. PcnHAK1.
BAB32444.1	AB055631	<i>Phragmites australis</i> high-affinity potassium transporter. PceHAK1A.
BAB32445.1	AB055632	<i>Phragmites australis</i> high-affinity potassium transporter. PceHAK1B.
BAB32442.1	AB055629	<i>Phragmites australis</i> high-affinity potassium transporter. PcuHAK1.
AAC39315.1	AF025292	<i>Hordeum vulgare</i> putative high-affinity potassium transporter. HvHAK1.
AAF36497.1	AF129485	<i>Oryza sativa</i> HAK4. HAK4; similar to <i>Hordeum vulgare</i> K ⁺ transporter HAK1.

AAF36496.1 AF129484 *Hordeum vulgare*
HAK4. HAK4. HvHAK4; similar to *Hordeum vulgare* K⁺ transporter HAK1.

CAC14883.1 AJ297888 *Hordeum vulgare*
putative potassium transporter. hak1.

CAC14787.1 AJ297886 *Hordeum vulgare*
putative potassium transporter. hak1.

AAF36492.1 AF129480 *Hordeum vulgare*
HAK1B. HAK1B. HvHAK1B; similar to *Hordeum vulgare* K⁺ transporter HAK1.

CAC15061.1 AJ300161 *Hordeum vulgare*
potassium transporter. hak4.

SEQ ID NO: 542

AAA91063.1 M88254 *Hevea brasiliensis*
ethylene-inducible protein. ER1.

SEQ ID NO: 546

CAA75386.1 Y15113 *Morinda citrifolia*
3-deoxy-D-arabino-heptulosonate 7-phosphate synthase. DS3. 2-dehydro-3-deoxyphosphoheptonate aldolase.

CAA79855.1 Z21792 *Lycopersicon esculentum*
phospho-2-dehydro-3-deoxyheptonate aldolase.

CAA79856.1 Z21793 *Lycopersicon esculentum*
phospho-2-dehydro-3-deoxyheptonate aldolase.

SEQ ID NO: 548

BAA96751.1 AP002521 *Oryza sativa*
Similar to *Arabidopsis thaliana* chromosome4, BAC clone T16H5; lectin like protein (AL024486).

SEQ ID NO: 551

BAB19096.1 AP002839 *Oryza sativa*
putative DNA-binding protein homolog. P0688A04.2.

BAB19075.1 AP002744 *Oryza sativa*
putative DNA-binding protein homolog. P0006C01.17.

AAK16170.1 AC079887 *Oryza sativa*
putative DNA binding protein. OSJNBA0040E01.4.

AAD32677.1 AF140554 *Avena sativa*
DNA-binding protein WRKY1. wrky1. putative transcription factor.

AAD16139.1 AF096299 *Nicotiana tabacum*
DNA-binding protein 2. WRKY2. transcription factor.

CAB97004.1 AJ278507 *Solanum tuberosum*
putative transcription factor. WRKY DNA binding protein. WRKY1.

CAA88326.1 Z48429 *Avena fatua*
binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.

AAC49527.1 U48831 *Petroselinum crispum*
WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.

AAC49529.1	U58540	Petroselinum crispum WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
AAK16171.1	AC079887	Oryza sativa putative DNA-binding protein. OSJNBa0040E01.10.
AAC37515.1	L44134	Cucumis sativus SPF1-like DNA-binding protein.
AAD16138.1	AF096298	Nicotiana tabacum DNA-binding protein 1. WRKY1. transcription factor.
AAD38283.1	AC007789	Oryza sativa putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAB18313.1	AP002865	Oryza sativa putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
BAB40073.1	AP003074	Oryza sativa putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
AAC49528.1	U56834	Petroselinum crispum DNA-binding. WRKY3. WRKY-type DNA-binding protein.
BAA77358.1	AB020023	Nicotiana tabacum WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.
AAG46150.1	AC018727	Oryza sativa putative DNA-binding protein. OSJNBa0056G17.18.
CAA88331.1	Z48431	Avena fatua binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAD32676.1	AF140553	Avena sativa DNA-binding protein WRKY3. wrky3. putative transcription factor.
CAB66338.1	AJ279697	Betula pendula wrky-type DNA binding protein. wrky.
AAF61863.1	AF193770	Nicotiana tabacum DNA-binding protein 3. WRKY3. transcription factor.
AAF61864.1	AF193771	Nicotiana tabacum DNA-binding protein 4. WRKY4. transcription factor.
AAD27591.1	AF121354	Petroselinum crispum binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.
BAA87069.1	AB035271	Matricaria chamomilla elicitor-induced DNA-binding protein homolog. McWRKY1.
SEQ ID NO: 553		
AAF34428.1	AF172282	Oryza sativa receptor-like protein kinase. DUPR11.18.
BAA94518.1	AP001800	Oryza sativa Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAB07904.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.12.

BAA94516.1	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07906.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.14.
BAA94517.1	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.13.
BAA94528.1	AP001800	Oryza sativa Similar to Arabidopsis thaliana chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).
BAA94529.2	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea serine /threonine kinase. ARLK.
CAB89179.1	AJ245479	Brassica napus subsp. napus ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus serine/threonine kinase receptor.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
BAA92836.1	AB032473	Brassica oleracea S18 S-locus receptor kinase. SRK18.
CAB41878.1	Y18259	Brassica oleracea SRK5 protein. SRK5. receptor-like kinase.
CAB41879.1	Y18260	Brassica oleracea SRK15 protein. SRK15. receptor-like kinase.
BAA21132.1	D88193	Brassica rapa S-receptor kinase. SRK9 (B.c.).
BAA06285.1	D30049	Brassica rapa S-receptor kinase SRK9.
CAA74662.1	Y14286	Brassica oleracea SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA79355.1	Z18921	Brassica oleracea S-receptor kinase-like protein.
BAB21001.1	AB054061	Brassica rapa S locus receptor kinase. SRK22.

AAA33915.1	L27821	Oryza sativa receptor type serine/threonine kinase. protein kinase.
BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
		SEQ ID NO: 554
CAC05658.1	AJ250919	Brassica napus endopolygalacturonase. pegaz.
CAC05657.1	AJ250918	Brassica napus endopolygalacturonase. pgaz.
CAA65072.1	X95800	Brassica napus polygalacturonase.
CAA90272.1	Z49971	Brassica napus Hydrolytic enzyme. Polygalacturonase. pga.
CAA54448.1	X77231	Prunus persica polygalacturonase. PG.
AAC14453.1	L12019	Actinidia deliciosa polygalacturonase.
AAF71160.1	AF152758	Actinidia chinensis polygalacturonase A. PGA.
AAA34178.1	M37304	Lycopersicon esculentum polygalacturonase.
CAA32235.1	X14074	Lycopersicon esculentum polygalacturonase.
CAA29148.1	X05656	Lycopersicon esculentum polygalacturonase (AA 1-457).
AAA32914.1	L06094	Persea americana cell wall degradation. polygalacturonase.
CAA47055.1	X66426	Persea americana polygalacturonase.
AAC26512.1	AF062467	Cucumis melo polygalacturonase precursor. MPG3.
CAA11846.1	AJ224147	Rubus idaeus polygalacturonase. RAS3.
AAF61444.1	AF138858	Lycopersicon esculentum hydrolyses polygalacturonic acid. polygalacturonase. XOPG1.
BAA88472.1	AB035890	Cucumis sativus polygalacturonase. CUPG1.
AAD46483.1	AF128266	Glycine max polygalacturonase PG1.
AAD46484.1	AF128267	Glycine max polygalacturonase PG2.

AAC28905.1 AF001002 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 4.
TAPG4. expressed in abscission.

AAC28906.1 AF001003 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 5.
TAPG5. expressed in abscission.

AAC28903.1 AF001000 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 1.
TAPG1. expressed in abscission.

AAA80489.1 U23053 *Lycopersicon esculentum*
polygalacturonase precursor.

AAC64184.1 AF095577 *Prunus persica*
endopolygalacturonase.

AAC28902.2 AF000999 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 3.
TAPG3. expressed in abscission.

AAB09575.1 U70480 *Lycopersicon esculentum*
abscission polygalacturonase. TAPG2.

AAC28904.1 AF001001 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 2.
TAPG2. expressed in abscission.

CAA54150.1 X76735 *Prunus persica*
endopolygalacturonase.

AAC70951.1 AF072732 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella. polygalacturonase 7. specifically and
abundantly expressed in pistils.

AAC26511.1 AF062466 *Cucumis melo*
polygalacturonase precursor. MPG2.

AAB09576.1 U70481 *Lycopersicon esculentum*
abscission polygalacturonase. TAPG4.

AAC28947.1 AF029230 *Lycopersicon esculentum*
polygalacturonase. TPG6.

AAA82167.1 U09717 *Gossypium hirsutum*
polygalacturonase.

AAA58322.1 U09805 *Gossypium barbadense*
polygalacturonase.

CAA47052.1 X66422 *Zea mays*
polygalacturonase. PG.

AAG14416.1 AF248538 *Nicotiana tabacum*
NTS1 protein. similar to polygalacturonase.

CAB42886.1 AJ238848 *Phleum pratense*
polygalacturonase. pg.

CAA40850.1	X57627	Zea mays polygalacturonase.
CAA46679.1	X65844	Zea mays polygalacturonase. PGg6.
CAA40910.1	X57743	Zea mays polygalacturonase.
CAA44249.1	X62385	Zea mays polygalacturonase.
CAA45751.1	X64408	Zea mays polygalacturonase. PG. pollen-preferentially expressed.
CAA40851.1	X57628	Zea mays polygalacturonase.
CAA46680.1	X65845	Zea mays polygalacturonase. PGg14.
AAC26510.1	AF062465	Cucumis melo polygalacturonase precursor. MPG1.
SEQ ID NO: 556		
CAA51734.1	X73301	Vigna mungo alpha-amylase. amyVm1.
CAA37217.1	X53049	Vigna mungo alpha-amylase (AA 1-421).
BAA33879.1	AB015131	Phaseolus vulgaris alpha-amylase.
AAA16513.1	U06754	Cuscuta reflexa starch hydrolysis. alpha amylase precursor. CUS AMY2.
AAA98615.1	J04202	Hordeum vulgare alpha-amylase. Amy46. precursor.
AAA98790.1	K02637	Hordeum vulgare alpha-amylase type B. Amy6-4. precursor.
CAA33298.1	X15226	Hordeum vulgare alpha-amylase.
AAA33885.1	M24286	Oryza sativa alpha-amylase (EC 3.2.1.1).
CAA34516.1	X16509	Oryza sativa alpha-amylase.
CAA72144.1	Y11277	Hordeum vulgare alpha-amylase. amy.
CAA33299.1	X15227	Hordeum vulgare alpha amylase.
AAA32925.1	M17126	Hordeum vulgare alpha-amylase 1.

AAA32927.1	M17128	Hordeum vulgare alpha-amylase 2.
AAA32929.1	J01236	Hordeum vulgare alpha-amylase type A, EC 3.2.1.1.
CAA39777.1	X56337	Oryza sativa alpha-amylase. RAmy3B.
CAA09323.1	AJ010728	Avena fatua alpha amylose. alpha-Amy2A.
AAA33897.1	M24941	Oryza sativa alpha-amylase precursor (EC 3.2.1.1).
CAA09324.1	AJ010729	Avena fatua alpha-amylase. alpha-Amy2D.
CAA28803.1	X05166	Hordeum vulgare alpha-amylase type A. Amy32b.
AAA32926.1	M17125	Hordeum vulgare alpha-amylase 1.
CAA39778.1	X56338	Oryza sativa alpha-amylase. RAmy3C.
AAA32935.1	M15208	Hordeum vulgare alpha-amylase.
AAA33895.1	M59351	Oryza sativa alpha-amylase. RAmy3D.
AAA33896.1	M59352	Oryza sativa alpha-amylase. RAmy3E.
AAA50161.1	L25805	Zea mays alpha-amylase.
AAA33894.1	M74177	Oryza sativa alpha-amylase. amy2A.
CAA72143.1	Y11276	Hordeum vulgare alpha-amylase. amy.
CAA39776.1	X56336	Oryza sativa alpha-amylase. RAmy3A.
CAA45903.1	X64619	Oryza sativa alpha-amylase. Amyc2. starts hydrolysis during seed germination.
AAA33886.1	M24287	Oryza sativa alpha-amylase (EC 3.2.1.1).
AAA32928.1	M17127	Hordeum vulgare alpha-amylase 2.
AAA32933.1	K02638	Hordeum vulgare pre-alpha-amylase type B, EC 3.2.1.1.
AAA91883.1	M81682	Solanum tuberosum alpha-amylase. Amy23.

AAA34259.1	M16991	Triticum aestivum alpha-amylase.
CAA29252.1	X05809	Triticum aestivum alpha-amylase.
AAA91884.1	M79328	Solanum tuberosum alpha-amylase.
AAF63239.1	AF153828	Malus x domestica degrades starch. alpha-amylase. alpha-amylase by similarity.
AAA32930.1	M10056	Hordeum vulgare alpha-amylase type B, EC 3.2.1.1.
AAA32931.1	K02635	Hordeum vulgare alpha-amylase type B, EC 3.2.1.1.
CAA36485.1	X52240	Oryza sativa alpha-amylase. OSamy-c.
AAA32932.1	K02636	Hordeum vulgare alpha-amylase type B, EC 3.2.1.1.
SEQ ID NO: 557		
CAA90272.1	Z49971	Brassica napus Hydrolytic enzyme. Polygalacturonase. pga.
CAA65072.1	X95800	Brassica napus polygalacturonase.
CAA67020.1	X98373	Brassica napus endo-polygalacturonidase.
CAC05658.1	AJ250919	Brassica napus endopolygalacturonase. pegaz.
CAC05657.1	AJ250918	Brassica napus endopolygalacturonase. pgaz.
AAC14453.1	L12019	Actinidia deliciosa polygalacturonase.
AAF71160.1	AF152758	Actinidia chinensis polygalacturonase A. PGA.
CAA54448.1	X77231	Prunus persica polygalacturonase. PG.
AAA34178.1	M37304	Lycopersicon esculentum polygalacturonase.
CAA29148.1	X05656	Lycopersicon esculentum polygalacturonase (AA 1-457).
CAA32235.1	X14074	Lycopersicon esculentum polygalacturonase.
AAA32914.1	L06094	Persea americana cell wall degradation. polygalacturonase.

CAA47055.1 X66426 *Persea americana*
polygalacturonase.

AAC26512.1 AF062467 *Cucumis melo*
polygalacturonase precursor. MPG3.

CAA11846.1 AJ224147 *Rubus idaeus*
polygalacturonase. RAS3.

BAA88472.1 AB035890 *Cucumis sativus*
polygalacturonase. CUPG1.

AAF61444.1 AF138858 *Lycopersicon esculentum*
hydrolyses polygalacturonic acid. polygalacturonase. XOPG1.

AAA80489.1 U23053 *Lycopersicon esculentum*
polygalacturonase precursor.

AAC28903.1 AF001000 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 1.
TAPG1. expressed in abscission.

AAB09575.1 U70480 *Lycopersicon esculentum*
abscission polygalacturonase. TAPG2.

AAC28904.1 AF001001 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 2.
TAPG2. expressed in abscission.

AAC28905.1 AF001002 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 4.
TAPG4. expressed in abscission.

AAC64184.1 AF095577 *Prunus persica*
endopolygalacturonase.

AAD46483.1 AF128266 *Glycine max*
polygalacturonase PG1.

AAC28906.1 AF001003 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 5.
TAPG5. expressed in abscission.

AAD46484.1 AF128267 *Glycine max*
polygalacturonase PG2.

CAAS4150.1 X76735 *Prunus persica*
endopolygalacturonase.

AAC26511.1 AF062466 *Cucumis melo*
polygalacturonase precursor. MPG2.

AAC28902.2 AF000999 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 3.
TAPG3. expressed in abscission.

AAC70951.1 AF072732 *Lycopersicon esculentum*
hydrolyzes pectin in the cell wall and middle lamella. polygalacturonase 7. specifically and
abundantly expressed in pistils.

CAA47052.1 X66422 Zea mays
polygalacturonase. PG.

AAC28947.1 AF029230 Lycopersicon esculentum
polygalacturonase. TPG6.

AAA82167.1 U09717 Gossypium hirsutum
polygalacturonase.

AAB09576.1 U70481 Lycopersicon esculentum
abscission polygalacturonase. TAPG4.

CAA40910.1 X57743 Zea mays
polygalacturonase.

CAA44249.1 X62385 Zea mays
polygalacturonase.

CAA40850.1 X57627 Zea mays
polygalacturonase.

AAG14416.1 AF248538 Nicotiana tabacum
NTS1 protein. similar to polygalacturonase.

CAA46679.1 X65844 Zea mays
polygalacturonase. PGg6.

AAC26510.1 AF062465 Cucumis melo
polygalacturonase precursor. MPG1.

AAA58322.1 U09805 Gossypium barbadense
polygalacturonase.

CAA46680.1 X65845 Zea mays
polygalacturonase. PGg14.

CAA40851.1 X57628 Zea mays
polygalacturonase.

CAA45751.1 X64408 Zea mays
polygalacturonase. PG. pollen-preferentially expressed.

CAB42886.1 AJ238848 Phleum pratense
polygalacturonase. pg.

SEQ ID NO: 559

CAB43937.1 AJ006348 Fragaria x ananassa
cell wall hydrolysis. endo-beta-1,4-glucanase. eg1.

AAC95009.1 AF074923 Fragaria x ananassa
endo-1,4-beta-glucanase precursor. Cell. 1,4-beta-glucanohydrolase.

AAC12684.1 U76725 Pinus radiata
endo-beta-1,4-glucanase. PrCell. cellulase; PRCEL1.

AAA69909.1 U13055 Lycopersicon esculentum
cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel2. cellulase.

CAA65600.1 X96856 Prunus persica
endo-beta-1,4-glucanase. ppEG1.

CAA65597.1	X96853	<i>Prunus persica</i> endo-beta-1,4-glucanase. pcel1.
CAA65827.1	X97189	<i>Capsicum annuum</i> endo-beta-1,4-glucanase. ccel3. cellulase.
AAC62241.1	AF077339	<i>Lycopersicon esculentum</i> endo-1,4-beta-glucanase. cel5. cellulase; also expressed in fruit and pistils.
BAA85150.1	AB032830	<i>Pisum sativum</i> endo-1,4-beta-glucanase. EGL2.
AAA80495.1	U20590	<i>Lycopersicon esculentum</i> endo-1,4-beta-glucanase precursor. cellulase.
BAB32662.1	AB055886	<i>Atriplex lentiformis</i> beta-1,4-glucanase. Al-cel1. cellulase.
CAA65828.1	X97190	<i>Capsicum annuum</i> endo-beta-1,4-glucanase. ccel2.
AAC12685.1	U76756	<i>Pinus radiata</i> endo-beta-1,4-glucanase. PrCel2. cellulase; PRCEL2.
BAA77239.1	AB025796	<i>Populus alba</i> endo-1,4-beta glucanase. POPCEL2. cellulase.
CAB59900.1	AJ010950	<i>Capsicum annuum</i> cell wall degradation. endo-beta-1,4-glucanase. eg2.
BAB39483.1	AB049200	<i>Populus alba</i> endo-1,4-beta-glucanase. PopCel2.
BAB39482.1	AB049199	<i>Populus alba</i> endo-1,4-beta glucanase. PopCell1.
CAA72133.1	Y11268	<i>Lycopersicon esculentum</i> endo-1,4-beta-D-glucanase. cel7.
AAA96135.1	L41046	<i>Pisum sativum</i> endo-1,4-beta-glucanase. EGL1.
AAC78504.1	U34754	<i>Phaseolus vulgaris</i> endo-1,4-beta-D-glucanase. cellulase.
AAA02563.1	M57400	<i>Phaseolus vulgaris</i> cellulase precursor. endo-1,4-beta-D-glucanase.
CAA60737.1	X87323	<i>Capsicum annuum</i> catalyzes hydrolysis of cell wall polysaccharides. cellulase. cel1. Beta-1,4-endoglycanohydrolase.
CAA65826.1	X97188	<i>Capsicum annuum</i> endo-beta-1,4-glucanase. ccel1. cellulase.
AAA69908.1	U13054	<i>Lycopersicon esculentum</i> cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel1. cellulase.
CAB43938.1	AJ006349	<i>Fragaria x ananassa</i> cell wall hydrolysis. endo-beta-1,4-glucanase. eg3.

BAA96209.1 AP002094	Oryza sativa
EST C72268(E1328)	corresponds to a region of the predicted gene. Similar to Fragaria x ananassa endo-beta-1,4-glucanase (AJ006349).
BAA96207.1 AP002094	Oryza sativa
EST C72268(E1328)	corresponds to a region of the predicted gene. Similar to Fragaria x ananassa endo-beta-1,4-glucanase (AJ006349).
AAD08699.1 AF098292	Lycopersicon esculentum endo-beta-1,4-D-glucanase. Cel18.
BAA94257.1 AB040769	Hordeum vulgare endo-1,4-beta-glucanase Cell1. Cell1.
AAC49704.1 U78526	Lycopersicon esculentum endo-1,4-beta-glucanase. Cel3.
CAB51903.1 AJ242807	Brassica napus endo-1,4-beta-D-glucanase. Cel16. cellulase.
AAA20082.1 U00730	Glycine max CMCase; cellulase; endo-1,4-beta-D-glucanase.
CAA11301.1 AJ223386	Fragaria x ananassa endo-beta-1,4-glucanase. faEG1. partial cDNA obtained by RT-PCR amplification.
CAA11302.1 AJ223387	Fragaria x ananassa endo-beta-1,4-glucanase. partial cDNA obtained by RT-PCR amplification.
BAA21111.1 D88417	Gossypium hirsutum endo-1,4-beta-glucanase.
AAA20083.1 U00731	Glycine max CMCase; cellulase; endo-1,4-beta-D-glucanase.
SEQ ID NO: 560	
AAB97617.1 U83687	Apium graveolens NADPH-dependent mannose 6-phosphate reductase. m6pr. aldo-keto reductase; similar to aldose 6-phosphate reductase also known as NADP-sorbitol-6-phosphate dehydrogenase encoded by GenBank Accession Number D11080.
AAC97607.1 AF057134	Malus x domestica synthesizes sorbitol, a major photosynthetic product in many members of the Rosaceae family. NADP-dependent sorbitol 6-phosphate dehydrogenase. S6PDH.
BAA01853.1 D11080	Malus x domestica NADP-dependent D-sorbitol-6-phosphate dehydrogenase. S6PDH.
SEQ ID NO: 561	
CAB43938.1 AJ006349	Fragaria x ananassa cell wall hydrolysis. endo-beta-1,4-glucanase. eg3.
BAA96209.1 AP002094	Oryza sativa
EST C72268(E1328)	corresponds to a region of the predicted gene. Similar to Fragaria x ananassa endo-beta-1,4-glucanase (AJ006349).
BAA96207.1 AP002094	Oryza sativa
EST C72268(E1328)	corresponds to a region of the predicted gene. Similar to Fragaria x ananassa endo-beta-1,4-glucanase (AJ006349).

AAD08699.1	AF098292	<i>Lycopersicon esculentum</i> endo-beta-1,4-D-glucanase. Cel8.
BAA21111.1	D88417	<i>Gossypium hirsutum</i> endo-1,4-beta-glucanase.
CAA65828.1	X97190	<i>Capsicum annuum</i> endo-beta-1,4-glucanase. ccel2.
CAB59900.1	AJ010950	<i>Capsicum annuum</i> cell wall degradation. endo-beta-1,4-glucanase. eg2.
AAC95009.1	AF074923	<i>Fragaria x ananassa</i> endo-1,4-beta-glucanase precursor. Cel1. 1,4-beta-glucanohydrolase.
CAB43937.1	AJ006348	<i>Fragaria x ananassa</i> cell wall hydrolysis. endo-beta-1,4-glucanase. eg1.
AAA80495.1	U20590	<i>Lycopersicon esculentum</i> endo-1,4-beta-glucanase precursor. cellulase.
BAA85150.1	AB032830	<i>Pisum sativum</i> endo-1,4-beta-glucanase. EGL2.
AAC12684.1	U76725	<i>Pinus radiata</i> endo-beta-1,4-glucanase. PrCell1. cellulase; PRCEL1.
BAB32662.1	AB055886	<i>Atriplex lentiformis</i> beta-1,4-glucanase. Al-cell1. cellulase.
AAC62241.1	AF077339	<i>Lycopersicon esculentum</i> endo-1,4-beta-glucanase. cel5. cellulase; also expressed in fruit and pistils.
CAA65826.1	X97188	<i>Capsicum annuum</i> endo-beta-1,4-glucanase. ccel1. cellulase.
AAA69909.1	U13055	<i>Lycopersicon esculentum</i> cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel2. cellulase.
CAA65597.1	X96853	<i>Prunus persica</i> endo-beta-1,4-glucanase. pcell.
CAA65600.1	X96856	<i>Prunus persica</i> endo-beta-1,4-glucanase. ppEG1.
AAC12685.1	U76756	<i>Pinus radiata</i> endo-beta-1,4-glucanase. PrCel2. cellulase; PRCEL2.
BAB39482.1	AB049199	<i>Populus alba</i> endo-1,4-beta glucanase. PopCell1.
CAA65827.1	X97189	<i>Capsicum annuum</i> endo-beta-1,4-glucanase. ccel3. cellulase.
BAB39483.1	AB049200	<i>Populus alba</i> endo-1,4-beta-glucanase. PopCel2.
BAA77239.1	AB025796	<i>Populus alba</i> endo-1,4-beta glucanase. POPCEL2. cellulase.
AAA69908.1	U13054	<i>Lycopersicon esculentum</i> cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel1. cellulase.

AAC78504.1	U34754	Phaseolus vulgaris endo-1,4-beta-D-glucanase. cellulase.
AAA02563.1	M57400	Phaseolus vulgaris cellulase precursor. endo-1,4-beta-D-glucanase.
CAA72133.1	Y11268	Lycopersicon esculentum endo-1,4-beta-D-glucanase. cel7.
AAA96135.1	L41046	Pisum sativum endo-1,4-beta-glucanase. EGL1.
CAB51903.1	AJ242807	Brassica napus endo-1,4-beta-D-glucanase. Cel16. cellulase.
AAC49704.1	U78526	Lycopersicon esculentum endo-1,4-beta-glucanase. Cel3.
BAA94257.1	AB040769	Hordeum vulgare endo-1,4-beta-glucanase Cell1. Cell1.
CAA11302.1	AJ223387	Fragaria x ananassa endo-beta-1,4-glucanase. partial cDNA obtained by RT-PCR amplification.
AAA20082.1	U00730	Glycine max CMCase; cellulase; endo-1,4-beta-D-glucanase.
CAA11301.1	AJ223386	Fragaria x ananassa endo-beta-1,4-glucanase. faEG1. partial cDNA obtained by RT-PCR amplification.
AAC64045.1	AF077340	Lycopersicon esculentum endo-1,4-beta-glucanase. cel5. cellulase.
SEQ ID NO: 562		
AAD53011.1	AF089848	Brassica napus senescence-specific cysteine protease. SAG12-1. BnSAG12-1.
AAD53012.1	AF089849	Brassica napus senescence-specific cysteine protease. SAG12-2. BnSAG12-2.
AAK27968.1	AF242372	Ipomoea batatas cysteine protease. SPCP1.
AAA50755.1	U13940	Alnus glutinosa cysteine proteinase. putative preprotein.
BAB13759.1	AB040454	Astragalus sinicus cysteine proteinase. AsNODf32. preprotein putative.
AAC62396.1	AF050756	Ricinus communis cysteine endopeptidase precursor. CysEP.
CAB09698.1	Z97022	Hordeum vulgare cysteine proteinase. putative.
CAA52425.1	X74406	Hemerocallis sp. thiol-protease. SEN102.
BAA83472.1	AB004648	Oryza sativa cysteine endopeptidase. RepA.

CAA56844.1	X80876	Oryza sativa cysteine protease.
BAA88898.1	AB020961	Zea mays cysteine protease component of protease-inhibitor complex. CPPIC.
AAC35211.1	U12637	Hemerocallis hybrid cultivar cysteine proteinase. SEN11.
CAB09697.1	Z97021	Hordeum vulgare cysteine endopeptidase EP-A. precursor.
AAB88263.1	AF019147	Zea mays cysteine proteinase Mir3. mir3.
AAD28477.1	AF133839	Sandersonia aurantiaca papain-like cysteine protease. PRT5. senescence-related.
CAB16317.1	Z99173	Nicotiana tabacum storage protein hydrolysis. cysteine proteinase precursor.
CAB09699.1	Z97023	Hordeum vulgare cysteine endopeptidase EP-A.
AAD10337.1	U94591	Hordeum vulgare cysteine proteinase precursor. EPA.
CAA06243.1	AJ004958	Pisum sativum thiol-protease. pre-pro-TPE4A protein. tpE4A.
CAB53515.1	AJ245924	Solanum tuberosum proteolysis. cysteine protease. cyp.
AAD48496.1	AF172856	Lycopersicon esculentum cysteine protease TDI-65. tdi-65. induced by drought; localized in the nuclei and chloroplast (Tabaeizadeh, Z. et al., 1995. Protoplasma, 186:208-219).
CAA05894.1	AJ003137	Lycopersicon esculentum cysteine protease. CYP1. C14.
AAA79915.1	U17135	Dianthus caryophyllus cysteine proteinase. DCCP1. expressed in senescent flower petals.
AAB37233.1	U34747	Phalaenopsis sp. SM9108 cysteine proteinase.
CAB17076.1	Z99954	Phaseolus vulgaris protein hydrolysis. cysteine proteinase precursor.
CAA84378.1	Z34895	Vicia sativa storage protein degradation. cysteine proteinase.
CAA53377.1	X75749	Vicia sativa storage protein hydrolysis. cysteine protease.
CAB17074.1	Z99952	Phaseolus vulgaris degradation of storage proteins. cysteine proteinase precursor.
AAB68374.1	U52970	Phaseolus vulgaris suggested to initiate phaseolin degradation during germination. cysteine endopeptidase 1. PvCEP-1.

CAA12118.1	AJ224766	<i>Phaseolus vulgaris</i> phaseolin degradation. cysteine protease.
AAC49455.1	U41902	<i>Pseudotsuga menziesii</i> cysteine protease. Pseudotzain. PM33cysP.
CAA46863.1	X66061	<i>Pisum sativum</i> thiolprotease. tpp. start codon ttg.
AAB41816.1	U44947	<i>Pisum sativum</i> NTH1. PsCyp1. cysteine protease homolog.
BAA83473.1	AB004819	<i>Oryza sativa</i> cysteine endopeptidase. Rep1.
BAA22544.1	D38532	<i>Ananas comosus</i> precursor of cysteine proteinase. FBSB precursor. stem bromelain precursor in fruit.
BAA11170.1	D76415	<i>Oryza sativa</i> cysteine proteinase.
AAD20453.1	AF099203	<i>Oryza sativa</i> cysteine endopeptidase precursor. EP3A.
CAA08860.1	AJ009829	<i>Ananas comosus</i> cysteine proteinase precursor, AN8. an8.
AAA85036.1	U19384	<i>Hordeum vulgare</i> cysteine proteinase EPB2 precursor.
AAA85035.1	U19359	<i>Hordeum vulgare</i> cysteine proteinase EPB1 precursor.

SEQ ID NO: 565

AAA97411.1	U51918	<i>Pisum sativum</i> pyruvate dehydrogenase E1 alpha subunit.
CAA81558.1	Z26949	<i>Solanum tuberosum</i> subunit of the mitochondrial pyruvate dehydrogenase complex. E1 alpha subunit of pyruvate dehydrogenase precursor.
AAC72195.1	AF069911	<i>Zea mays</i> pyruvate dehydrogenase E1 alpha subunit.
AAG43499.1	AF209924	<i>Lycopersicon esculentum</i> pyruvate dehydrogenase.
CAB08111.1	Z94180	<i>Lycopersicon esculentum</i> branched chain alpha-keto acid dehydrogenase E1-alpha subunit.

SEQ ID NO: 566

AAD55090.1	AF178653	<i>Vitis riparia</i> thaumatin. osmotin; pathogenesis-related protein.
CAA51432.1	X72928	<i>Solanum commersonii</i> osmotin-like protein.
CAA47601.1	X67121	<i>Solanum commersonii</i> osmotin-like protein.
CAC34055.1	AJ297410	<i>Capsicum annuum</i> osmotin-like protein. pr5 p23.

CAA47047.1	X66416	Lycopersicon esculentum tpm 1. Induced during viroid infection. Osmotin-like, antifungal protein homologue.
AAB23375.1	S44889	Nicotiana tabacum osmotin. osmotin. pathogenesis-related protein homolog; This sequence comes from Fig. 3.
AAB22459.2	S40046	Nicotiana tabacum osmotin. abscisic acid-activated. basic PR-like protein; This sequence comes from Fig. 1A; conceptual translation presented here differs from translation in publication; mismatch(181[R->G]).
AAG16625.1	AY007309	Solanum dulcamara cryoprotective osmotin-like protein.
CAA46623.1	X65701	Nicotiana tabacum osmotin. AP24.
CAA46622.1	X65700	Nicotiana tabacum osmotin. AP24.
CAA51431.1	X72927	Solanum commersonii osmotin-like protein.
CAA64620.1	X95308	Nicotiana tabacum PR protein. osmotin.
CAA51430.1	X72926	Solanum commersonii osmotin-like protein.
AAC64171.1	AF093743	Lycopersicon esculentum pathogenesis-related protein osmotin precursor. NP24.
AAB61590.1	AF003007	Vitis vinifera VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.
BAA11180.1	D76437	Nicotiana sylvestris antifungal activity. neutral PR-5 (osmotin-like protein, PR-5d). neutral isoform of pathogenesis-related protein group 5.
AAA34087.1	M64081	Nicotiana tabacum osmotin-like protein. OLP1.
CAA47669.1	X67244	Solanum commersonii osmotin-like protein.
CAA71883.1	Y10992	Vitis vinifera osmotin-like protein. OSM1.
AAF13707.1	AF199508	Fragaria x ananassa osmotin-like protein. olp.
AAA34089.1	M29279	Nicotiana tabacum osmotin.
CAA43854.1	X61679	Nicotiana tabacum osmotin.
CAA04642.1	AJ001268	Hordeum vulgare antifungal. basic pathogenesis-related protein PR5. osmotin/permatin-like.
CAC22330.1	AJ298304	Fagus sylvatica stress protein. osmotin-like protein. olp2.

CAC22329.1 AJ298303 *Fagus sylvatica*
stress protein. osmotin-like protein. olp.

AAB67852.1 L76377 *Oryza sativa*
osmotin. 14b.

CAB36911.1 AJ000692 *Quercus suber*
stress protein. osmotin-like protein. olp.

SEQ ID NO: 569

BAA95814.1 AP002069 *Oryza sativa*

ESTs AU082579(S2069),D40238(S2069) correspond to a region of the predicted gene.
Similar to *Arabidopsis thaliana* vesicle-associated membrane protein 7C; synaptobrevin 7C.
(AF025332).

SEQ ID NO: 572

AAA92677.1 U13736 *Pisum sativum*
binds calcium. calmodulin-like protein.

AAA34015.1 L01433 *Glycine max*
calcium-binding regulatory protein. calmodulin. SCaM-4. putative.

AAA33948.1 L19359 *Glycine max*
calcium-binding regulatory protein. calmodulin. SCaM-5. putative.

CAA66159.1 X97558 *Capsicum annuum*
calmodulin-1.

CAA09302.1 AJ010645 *Capsicum annuum*
calcium binding protein. calmodulin 3 protein. calmodulin 3.

AAA34144.1 M67472 *Lycopersicon esculentum*
calmodulin. CALM1LE.

CAA62150.1 X90560 *Physcomitrella patens*
Calmodulin. CaM.

AAB46588.1 U83402 *Capsicum annuum*
calmodulin.

BAA87825.1 AP000815 *Oryza sativa*
ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene.
Similar to *O.sativa* gene encoding calmodulin. (Z12828).

AAF65511.1 AF108889 *Capsicum annuum*
calmodulin.

AAA85157.1 U20297 *Solanum tuberosum*
calcium-binding protein. calmodulin.

AAA85156.1 U20296 *Solanum tuberosum*
calcium-binding protein. calmodulin.

AAA62351.1 U20295 *Solanum tuberosum*
calcium-binding protein. calmodulin.

AAA85155.1 U20294 *Solanum tuberosum*
calcium-binding protein. calmodulin.

AAA33900.1 L18914 *Oryza sativa*
calcium binding protein, signal transduction. calmodulin.

CAA78288.1	Z12828	Oryza sativa calcium binding protein, signal transduction. calmodulin.
AAC49583.1	U48692	Triticum aestivum calmodulin TaCaM2-3. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum calmodulin TaCaM2-2. calcium-binding protein.
CAA61980.1	X89890	Bidens pilosa Calmodulin.
CAA67054.1	X98404	Capsicum annuum calmodulin-2.
AAA33083.1	M20729	Chlamydomonas reinhardtii calmodulin.
AAG11418.1	AF292108	Prunus avium calmodulin.
AAF33852.1	AF231026	Oryza sativa calmodulin-like protein.
AAA92681.1	U13882	Pisum sativum calcium-binding protein. calmodulin.
AAA33706.1	M80836	Petunia x hybrida calmodulin. CAM81.
AAA33705.1	M80831	Petunia x hybrida calmodulin-related protein. CAM53.
AAA98933.1	U37936	Oryza sativa novel calmodulin-like protein. C-terminal of this sequence contains a CAAX box which is common in signal transport protein, but not in calmodulin.
CAA43143.1	X60738	Malus x domestica Calmodulin. CaM.
CAA78301.1	Z12839	Lilium longiflorum calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	Lilium longiflorum calcium binding protein, signal transduction. calmodulin. putative.
CAA42423.1	X59751	Daucus carota calmodulin. Ccam-1.
AAF73157.1	AF150059	Brassica napus calmodulin. CaM1. involved in seed germination.
AAA19571.1	U10150	Brassica napus calcium binding. calmodulin. bcml.
AAA87347.1	M88307	Brassica juncea calmodulin.
AAG27432.1	AF295637	Elaeis guineensis calmodulin.
BAA94697.1	AB041712	Chara corallina calmodulin. cccam2.

BAA94696.1 AB041711 Chara corallina
calmodulin. cccam1.

BAA96536.1 AB044286 Chara corallina
calmodulin. ccam.

AAC18355.1 AF064456 Oryza sativa subsp. indica
calmodulin-like protein. CAM-like.

AAA34237.1 L20691 Vigna radiata
calmodulin.

CAA52602.1 X74490 Zea mays
Calmodulin. ZMCALM1.

CAA54583.1 X77397 Zea mays
calmodulin. CaM2.

AAC49585.1 U49103 Triticum aestivum
calmodulin TaCaM3-2. calcium-binding protein.

AAC49586.1 U49104 Triticum aestivum
calmodulin TaCaM3-3. calcium-binding protein.

AAC49587.1 U49105 Triticum aestivum
calmodulin TaCaM4-1. calcium-binding protein.

AAC49580.1 U48689 Triticum aestivum
calmodulin TaCaM1-3. calcium-binding protein.

AAC49584.1 U48693 Triticum aestivum
calmodulin TaCaM3-1. calcium-binding protein.

SEQ ID NO: 575

AAK28303.1 AF346431 Nicotiana tabacum
phenylpropanoid:glucosyltransferase 1. tog1. glucosyltransferase.

AAB36653.1 U32644 Nicotiana tabacum
immediate-early salicylate-induced glucosyltransferase. IS5a.

AAB36652.1 U32643 Nicotiana tabacum
immediate-early salicylate-induced glucosyltransferase. IS10a.

AAK28304.1 AF346432 Nicotiana tabacum
phenylpropanoid:glucosyltransferase 2. tog2. glucosyltransferase.

CAA59450.1 X85138 Lycopersicon esculentum
tw1. homologous to glucosyltransferases.

CAB56231.1 Y18871 Dorotheanthus bellidiformis
betanidin-5-O-glucosyltransferase.

BAA83484.1 AB031274 Scutellaria baicalensis
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

AAB48444.1 U82367 Solanum tuberosum
UDP-glucose glucosyltransferase.

CAA54610.1 X77460 Manihot esculenta
UTP-glucose glucosyltransferase. CGT4.

AAD04166.1 AF101972 *Phaseolus lunatus*
catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

BAB17182.1 AP002843 *Oryza sativa*
putative UTP-glucose glucosyltransferase. P0407B12.19.

BAA93039.1 AB033758 *Citrus unshiu*
limonoid UDP-glucosyltransferase. LGTase.

AAF61647.1 AF190634 *Nicotiana tabacum*
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAB17176.1 AP002843 *Oryza sativa*
putative UTP-glucose glucosyltransferase. P0407B12.13.

CAC09351.1 AL442007 *Oryza sativa*
putative glucosyltransferase. H0212B02.7.

CAA54611.1 X77461 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT2.

AAF98390.1 AF287143 *Brassica napus*
catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeoate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

AAK16181.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.16.

AAK16178.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.5.

CAA54612.1 X77462 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT5.

AAK16180.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.21.

AAF17077.1 AF199453 *Sorghum bicolor*
UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.

CAA54609.1 X77459 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT1.

BAB41025.1 AB047098 *Vitis vinifera*
UDP-glucose:flavonoid 3-O-glucosyltransferase. FlUFGT1.

AAK16172.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.14.

BAB41019.1 AB047092 *Vitis vinifera*
UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.

BAB41018.1 AB047091 *Vitis labrusca x Vitis vinifera*
UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents *V. vinifera* cv. Centennial.

BAB41023.1 AB047096	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. A1UFGT1.
BAB41021.1 AB047094	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAA89009.1 AB027455	Petunia x hybrida anthocyanin 5-O-glucosyltransferase. PH1.
AAB81682.1 AF000371	Vitis vinifera UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41017.1 AB047090	Vitis labrusca x Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
BAB41022.1 AB047095	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41020.1 AB047093	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAB41024.1 AB047097	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. A1UFGT2.
AAB81683.1 AF000372	Vitis vinifera UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41026.1 AB047099	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
CAA54613.1 X77463	Manihot esculenta UTP-glucose glucosyltransferase. CGT6.
BAA89008.1 AB027454	Petunia x hybrida anthocyanidin 3-O-glucosyltransferase. PGT8.
BAA12737.1 D85186	Gentiana triflora UDP-glucose:flavonoid-3-glucosyltransferase.
SEQ ID NO: 576	
CAB60277.1 AJ002586	Solanum tuberosum UCP.
CAA72107.1 Y11220	Solanum tuberosum mitochondrial uncoupling protein.
BAA92172.1 AB024733	Symplocarpus renifolius SfUCPa. SfUCPa.
BAB40658.1 AB049998	Oryza sativa uncoupling protein. OsUCP2.
BAA92173.1 AB024734	Symplocarpus renifolius SfUCPb. SfUCPb.
BAB16385.1 AB042429	Triticum aestivum uncoupling protein. WhUCP1b.
BAB16384.1 AB042428	Triticum aestivum uncoupling protein. WhUCP1a.

BAB40657.1 AB049997 *Oryza sativa*
uncoupling protein. OsUCP1.

SEQ ID NO: 577

AAA19571.1 U10150 *Brassica napus*
calcium binding. calmodulin. bcm1.

AAA87347.1 M88307 *Brassica juncea*
calmodulin.

AAA92681.1 U13882 *Pisum sativum*
calcium-binding protein. calmodulin.

AAA33706.1 M80836 *Petunia x hybrida*
calmodulin. CAM81.

CAA43143.1 X60738 *Malus x domestica*
Calmodulin. CaM.

CAA78301.1 Z12839 *Lilium longiflorum*
calcium binding protein, signal transduction. calmodulin.

AAA33397.1 L18912 *Lilium longiflorum*
calcium binding protein, signal transduction. calmodulin. putative.

CAA42423.1 X59751 *Daucus carota*
calmodulin. Ccam-1.

AAG27432.1 AF295637 *Elaeis guineensis*
calmodulin.

AAG11418.1 AF292108 *Prunus avium*
calmodulin.

AAA34237.1 L20691 *Vigna radiata*
calmodulin.

AAC49587.1 U49105 *Triticum aestivum*
calmodulin TaCaM4-1. calcium-binding protein.

AAC49586.1 U49104 *Triticum aestivum*
calmodulin TaCaM3-3. calcium-binding protein.

AAC49585.1 U49103 *Triticum aestivum*
calmodulin TaCaM3-2. calcium-binding protein.

AAC49584.1 U48693 *Triticum aestivum*
calmodulin TaCaM3-1. calcium-binding protein.

AAC49580.1 U48689 *Triticum aestivum*
calmodulin TaCaM1-3. calcium-binding protein.

AAC49579.1 U48688 *Triticum aestivum*
calmodulin TaCaM1-2. calcium binding protein.

AAC49578.1 U48242 *Triticum aestivum*
calmodulin TaCaM1-1. calcium-binding.

AAA03580.1 L01431 *Glycine max*
calcium-binding regulatory protein. calmodulin. SCaM-2. putative.

AAB36130.1	S81594	Vigna radiata
auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.		
AAA33901.1	L18913	Oryza sativa
calcium binding protein, signal transduction. calmodulin. putative.		
CAA78287.1	Z12827	Oryza sativa
calcium binding protein, signal transduction. calmodulin.		
AAB46588.1	U83402	Capsicum annuum
calmodulin.		
AAA32938.1	M27303	Hordeum vulgare
calmodulin.		
BAA88540.1	AP000969	Oryza sativa
ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).		
AAF65511.1	AF108889	Capsicum annuum
calmodulin.		
AAC36059.1	AF042840	Oryza sativa
calmodulin. CaM1.		
AAA34238.1	L20507	Vigna radiata
calmodulin.		
AAA34014.1	L01432	Glycine max
calcium-binding regulatory protein. calmodulin. SCaM-3. putative.		
AAA34013.1	L01430	Glycine max
calcium-binding regulatory protein. calmodulin. SCaM-1. putative.		
CAA36644.1	X52398	Medicago sativa
calmodulin (AA 1-149).		
AAB68399.1	U79736	Helianthus annuus
calmodulin. HaCaM.		
AAD10244.1	AF030032	Phaseolus vulgaris
calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.		
AAA33705.1	M80831	Petunia x hybrida
calmodulin-related protein. CAM53.		
AAA16320.1	L14071	Bryonia dioica
calmodulin. Bc329. calcium-binding sites (amino acid #): 1. (21..33); 2. (57..68); 3. (94..106); 4. (130..141).		
CAA61980.1	X89890	Bidens pilosa
Calmodulin.		
AAA33900.1	L18914	Oryza sativa
calcium binding protein, signal transduction. calmodulin.		
CAA78288.1	Z12828	Oryza sativa
calcium binding protein, signal transduction. calmodulin.		

CAA74307.1	Y13974	Zea mays calmodulin.
AAC49583.1	U48692	Triticum aestivum calmodulin TaCaM2-3. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum calmodulin TaCaM2-2. calcium-binding protein.
AAA85157.1	U20297	Solanum tuberosum calcium-binding protein. calmodulin.
AAA85156.1	U20296	Solanum tuberosum calcium-binding protein. calmodulin.
AAA62351.1	U20295	Solanum tuberosum calcium-binding protein. calmodulin.
AAA85155.1	U20294	Solanum tuberosum calcium-binding protein. calmodulin.
CAA46150.1	X65016	Oryza sativa calmodulin. cam.
AAD10246.1	AF030034	Phaseolus vulgaris calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
AAF73157.1	AF150059	Brassica napus calmodulin. CaM1. involved in seed germination.
CAA54583.1	X77397	Zea mays calmodulin. CaM2.
SEQ ID NO: 578		
AAF01764.2	AF184277	Glycine max homeodomain-leucine zipper protein 56. Hdl56. transcription factor.
BAA21017.1	D26578	Daucus carota transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.
AAD37697.1	AF145728	Oryza sativa homeodomain leucine zipper protein. Oshox4. transcription factor.
CAB67118.1	Y17306	Lycopersicon esculentum homeodomain protein. h52.
AAF01765.1	AF184278	Glycine max homeodomain-leucine zipper protein 57. Hdl57. transcription factor.
BAA05624.1	D26575	Daucus carota transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.
BAA93466.1	AB028078	Physcomitrella patens homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.
BAA93465.1	AB028077	Physcomitrella patens homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.

BAA93464.1	AB028076	<i>Physcomitrella patens</i> homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.
BAA05622.1	D26573	<i>Daucus carota</i> transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.
BAA05625.1	D26576	<i>Daucus carota</i> transcriptiional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.
BAA05623.1	D26574	<i>Daucus carota</i> trancsriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.
AAD37698.1	AF145729	<i>Oryza sativa</i> homeodomain leucine zipper protein. Oshox5. transcription factor.
BAA93461.1	AB028073	<i>Physcomitrella patens</i> homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.
BAA93467.1	AB028079	<i>Physcomitrella patens</i> homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.
BAA93468.1	AB028080	<i>Physcomitrella patens</i> homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.
BAA93460.1	AB028072	<i>Physcomitrella patens</i> homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.
AAD37699.1	AF145730	<i>Oryza sativa</i> homeodomain leucine zipper protein. Oshox6. transcription factor.
CAA06717.1	AJ005820	<i>Craterostigma plantagineum</i> transcription factor. homeodomain leucine zipper protein. hb-1.
BAA93463.1	AB028075	<i>Physcomitrella patens</i> homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
CAA65456.2	X96681	<i>Oryza sativa</i> transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.
AAF19980.1	AF211193	<i>Oryza sativa</i> homeodomain-leucine zipper transcription factor. Hox1. hox1.
AAK31270.1	AC079890	<i>Oryza sativa</i> homeodomain leucine zipper protein hox1. OSJNBb0089A17.12.
CAA06728.1	AJ005833	<i>Craterostigma plantagineum</i> transcription factor. homeodomain leucine zipper protein. hb-2.
AAD37696.1	AF145727	<i>Oryza sativa</i> homeodomain leucine zipper protein. Oshox3. transcription factor.
SEQ ID NO: 580		
AAD32141.1	AF123503	<i>Nicotiana tabacum</i> Nt-gh3 deduced protein.
CAA42636.1	X60033	<i>Glycine max</i> auxin-responsive GH3 product. GH3.

BAA96221.1	AP002094	Oryza sativa
ESTs C19814(E10971),AU090481(E10971) correspond to a region of the predicted gene.		
Similar to <i>Arabidopsis thaliana</i> chromosome 2, sequence from clones T3F17, F11C10, F13A10; auxin-responsive GH3-like protein (AC006526).		
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SEQ ID NO: 581		
AAD13632.1	AF059488	<i>Lycopersicon esculentum</i> expansin precursor. Exp4.
AAF32410.1	AF230277	<i>Triphysaria versicolor</i> alpha-expansin 2.
CAA04385.1	AJ000885	<i>Brassica napus</i> Cell wall extension in plants. Expansin.
CAB46492.1	AJ243340	<i>Lycopersicon esculentum</i> expansin9. exp9.
AAC63088.1	U82123	<i>Lycopersicon esculentum</i> expansin. LeEXP1. fruit ripening regulated expansin.
CAA06271.2	AJ004997	<i>Lycopersicon esculentum</i> expansin18. exp18.
AAF62182.1	AF247164	<i>Oryza sativa</i> alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.
AAF35900.1	AF230331	<i>Zinnia elegans</i> expansin. Exp1.
AAG13982.1	AF297521	<i>Prunus avium</i> expansin 1. Exp1. PruavExp1.
AAC33529.1	U93167	<i>Prunus armeniaca</i> expansin. PA-Exp1.
AAF21101.1	AF159563	<i>Fragaria x ananassa</i> expansin. Exp2. ripening regulated.
AAF35901.1	AF230332	<i>Zinnia elegans</i> expansin 2.
AAG13983.1	AF297522	<i>Prunus avium</i> expansin 2. Exp2. PruavExp2.
AAC33530.1	AF038815	<i>Prunus armeniaca</i> expansin. Exp2.
BAB19676.1	AB029083	<i>Prunus persica</i> expansin. PchExp1.
AAB40637.1	U64893	<i>Pinus taeda</i> expansin. similar to <i>Arabidopsis</i> expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to <i>Cucumis sativus</i> expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAB37746.1	U30382	<i>Cucumis sativus</i> expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, <i>Lolium perenne</i> , Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.

CAC19184.1	AJ291817	<i>Cicer arietinum</i>
		expansin.
AAD47901.1	AF085330	<i>Pinus taeda</i>
		expansin.
AAB40634.1	U64890	<i>Pinus taeda</i>
		expansin. similar to <i>Arabidopsis</i> expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to <i>Cucumis sativus</i> expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAF32409.1	AF230276	<i>Triphysaria versicolor</i>
		alpha-expansin 3.
AAC39512.1	AF043284	<i>Gossypium hirsutum</i>
		expansin. GhEX1. contains N-terminal signal peptide.
AAB40635.1	U64891	<i>Pinus taeda</i>
		expansin. similar to <i>Arabidopsis</i> expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to <i>Cucumis sativus</i> expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAC96081.1	AF049354	<i>Nicotiana tabacum</i>
		involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.
AAB38074.1	U30477	<i>Oryza sativa</i>
		induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.
AAG32921.1	AF184233	<i>Lycopersicon esculentum</i>
		expansin. Exp10.
AAB81662.1	U85246	<i>Oryza sativa</i>
		expansin. Os-EXP4.
AAD49956.1	AF167360	<i>Rumex palustris</i>
		expansin. EXP1.
AAB40636.1	U64892	<i>Pinus taeda</i>
		expansin. similar to <i>Arabidopsis</i> expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to <i>Cucumis sativus</i> expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAF32411.1	AF230278	<i>Triphysaria versicolor</i>
		alpha-expansin 1.
AAC96080.1	AF049353	<i>Nicotiana tabacum</i>
		involved in acid-growth response. alpha-expansin precursor. Nt-EXP4. cell wall protein.
AAF35902.1	AF230333	<i>Zinnia elegans</i>
		expansin 3.
CAB43197.1	AJ239068	<i>Lycopersicon esculentum</i>
		cell wall loosening enzyme. expansin2. exp2.
AAC64201.1	AF096776	<i>Lycopersicon esculentum</i>
		expansin. LeEXP2.

AAF17570.1	AF202119	Marsilea quadrifolia alpha-expansin. EXP1. Mq-EXP1.
AAD13633.1	AF059489	Lycopersicon esculentum expansin precursor. Exp5.
AAF62181.1	AF247163	Oryza sativa alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.
AAF17571.1	AF202120	Regnellidium diphyllum alpha-expansin. EXP1. Rd-EXP1.
AAF62180.1	AF247162	Oryza sativa alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.
CAC19183.1	AJ291816	Cicer arietinum expansin.
CAC06433.1	AJ276007	Festuca pratensis expansin. exp2.
BAB32732.1	AB049406	Eustoma grandiflorum expansin. Eg Expansin.
AAG01875.1	AF291659	Striga asiatica alpha-expansin 3. Exp3.
AAB37749.1	U30460	Cucumis sativus expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAC96077.1	AF049350	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
AAC96079.1	AF049352	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
AAG32920.1	AF184232	Lycopersicon esculentum expansin. Exp8.
CAA69105.1	Y07782	Oryza sativa expansin. RiExA.
AAC96078.1	AF049351	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
SEQ ID NO: 583		
BAA85412.1	AP000615	Oryza sativa ESTs AU065232(E60855), C23624(S1554), AU078241(E60855) correspond to a region of the predicted gene.; similar to putative adenylate kinase. (AC005896).
BAA01181.1	D10335	Oryza sativa adenylate kinase-b. Adk-b.
BAA01180.1	D10334	Oryza sativa adenylate kinase-a. Adk-a.
BAA94761.1	AB041773	Oryza sativa adenylate kinase. Adk-a.

AAB68604.1	U82330	Prunus armeniaca adenylate kinase homolog.
AAF23372.1	AF187063	Oryza sativa catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase b. ura6.
AAF23371.1	AF187062	Oryza sativa catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase a. ura6.
AAD41679.1	AF086603	Ceratopteris richardii adenylate kinase. ADK1.
BAA85443.1	AP000616	Oryza sativa similar to UMP/CMP kinase (AF000147).
SEQ ID NO: 584		
BAA87052.2	D88273	Hordeum vulgare nicotianamine aminotransferase A. naat-A.
BAA87055.1	AB024006	Hordeum vulgare nicotianamine aminotransferase. naat-A.
BAA87053.1	AB005788	Hordeum vulgare nicotianamine aminotransferase B. naat-b. NAAT-B.
BAA87054.1	AB024006	Hordeum vulgare nicotianamine aminotransferase. naat-B.
BAA77261.1	AB007405	Oryza sativa alanine aminotransferase. AlaAT.
BAA77260.1	AB007404	Oryza sativa alanine aminotransferase. AlaAT.
CAA49199.1	X69421	Panicum miliaceum alanine aminotransferase. pAlaAT-2.
AAB01685.1	U31975	Chlamydomonas reinhardtii catalyzes the transfer of -NH2 from ala to 2-oxoglutarate. alanine aminotransferase. The translation start site has not been experimentally tested, but a 55 kDa product can be detected in Western blot.
AAC62456.1	AF055898	Zea mays alanine aminotransferase. alt. AlaAT.
CAA81231.1	Z26322	Hordeum vulgare alanine aminotransferase.
SEQ ID NO: 586		
AAB94589.1	AF022460	Glycine max CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.
AAA32913.1	M32885	Persea americana cytochrome P-450LXXIA1 (cyp71A1).
AAA19701.1	L24438	Thlaspi arvense cytochrome P450.

BAB40324.1	AB037245	Asparagus officinalis cytochrome P450. ASPI-2.
AAC39318.1	AF029858	Sorghum bicolor second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldioxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.
BAB40323.1	AB037244	Asparagus officinalis cytochrome P450. ASPI-1.
CAA71517.1	Y10493	Glycine max putative cytochrome P450.
AAB61965.1	U48435	Solanum chacoense putative cytochrome P450.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
AAB61964.1	U48434	Solanum chacoense putative cytochrome P450.
AAD47832.1	AF166332	Nicotiana tabacum cytochrome P450.
AAB94588.1	AF022459	Glycine max CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAF27282.1	AF122821	Capsicum annuum cytochrome P450. PepCYP.
CAA50312.1	X70981	Solanum melongena P450 hydroxylase. CYPEG2.
CAA83941.1	Z33875	Mentha x piperita cytochrome P-450 oxidase.
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
CAA70576.1	Y09424	Nepeta racemosa cytochrome P450. CYP71A6.
AAD44151.1	AF124816	Mentha x piperita cytochrome p450 isoform PM17.
BAA03635.1	D14990	Solanum melongena Cytochrome P-450EG4.
CAA50645.1	X71654	Solanum melongena P450 hydroxylase.
AAB69644.1	AF000403	Lotus japonicus putative cytochrome P450. LjNP450.
AAD37433.1	AF150881	Lycopersicon esculentum x Lycopersicon peruvianum catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.

CAA65580.1	X96784	Nicotiana tabacum cytochrome P450. hsr515.
AAD44152.1	AF124817	Mentha x piperita cytochrome p450 isoform PM2.
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
AAG14962.1	AF214008	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H2.
AAG14961.1	AF214007	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H1.
CAB56503.1	AJ238612	Catharanthus roseus cytochrome P450.
AAG14963.1	AF214009	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H3.
AAK38088.1	AF321864	Lolium rigidum putative cytochrome P450.
AAD44150.1	AF124815	Mentha spicata cytochrome p450.
AAK38084.1	AF321860	Lolium rigidum putative cytochrome P450.
AAD56282.1	AF155332	Petunia x hybrida flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAK38087.1	AF321863	Lolium rigidum putative cytochrome P450.
AAK38083.1	AF321859	Lolium rigidum putative cytochrome P450.
AAB94584.1	AF022157	Glycine max capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
CAA71514.1	Y10490	Glycine max putative cytochrome P450.
BAA12159.1	D83968	Glycine max Cytochrome P-450 (CYP93A1).
BAB39252.1	AP002968	Oryza sativa putative cytochrome P450. P0416G11.1.
CAA50155.1	X70824	Solanum melongena flavonoid hydroxylase (P450). CYP75.
SEQ ID NO: 587		
CAA60120.1	X86222	Pisum sativum heat shock protein. hsp22.
AAF37726.1	AF237957	Euphorbia esula LMW heat shock protein. putative 22 kDa mitochondrial heat shock protein.

BAA32547.1	AB017134	<i>Lycopersicon esculentum</i> mitochondrial small heat shock protein. LEMTSHP.
CAA33388.1	X15333	<i>Chenopodium rubrum</i> heat shock protein (AA 1-204).
AAB03096.1	U21722	<i>Glycine max</i> Hsp23.9. Gmhsp23.9. low molecular weight heat shock protein.
AAC12279.1	AF035460	<i>Zea mays</i> low molecular weight heat shock protein precursor. hsp22.
AAD03604.1	AF104107	<i>Triticum aestivum</i> small heat shock protein Hsp23.5. mRNA not present, or only at very low levels, prior to heat stress; mRNA abundant after two hours at 40C.
AAB01557.1	L47741	<i>Picea glauca</i> mitochondria-localized low molecular weight heat shock protein 23.5. EMB22, SMW HSP23.5.
AAD03605.1	AF104108	<i>Triticum aestivum</i> small heat shock protein Hsp23.6.
CAA38037.1	X54103	<i>Plastid Petunia x hybrida</i> heat shock protein. hsp21.
AAF19022.1	AF197942	<i>Funaria hygrometrica</i> chloroplast-localized small heat shock protein 22. CPsHSP22.
AAB49626.1	U59917	<i>Lycopersicon esculentum</i> chromoplast-associated hsp20. pTOM111. small molecular weight heat shock protein.
AAB07023.1	U66300	<i>Chloroplast Lycopersicon esculentum</i> heat shock protein. HSP21.
BAA29064.1	D88584	<i>Nicotiana tabacum</i> heat shock protein 26 (Type I). Nthsp26a. plastid-localized small heat shock protein.
AAF19021.1	AF197941	<i>Funaria hygrometrica</i> chloroplast-localized small heat shock protein. CPsHSP21. CPsHS 21.
BAA78385.1	AB020973	<i>Oryza sativa</i> heat shock protein 26. Oshsp26. chloroplast-localized small heat shock protein.
CAA41219.1	X58280	<i>Triticum aestivum</i> heat shock protein 26.6. Tahsp26.6.
AAC96315.1	AF097657	<i>Triticum aestivum</i> heat shock protein HSP26. hsp26.6. similar to the <i>Triticum aestivum</i> hsp26.6G2 protein encoded by the sequence presented in GenBank Accession Number L41503; 26 kDa protein.
AAC96316.1	AF097658	<i>Triticum aestivum</i> heat shock protein HSP26. hsp26.6. 26 kDa protein.
AAC96314.1	AF097656	<i>Triticum aestivum</i> heat shock protein HSP26. hsp26.6. 26 kDa protein.
CAA47745.1	X67328	<i>Triticum aestivum</i> heat shock protein 26.6B. hsp 26.6B.
AAC96317.1	AF097659	<i>Triticum aestivum</i> heat shock protein HSP26. hsp26.6. 26 kDa protein.

AAA33477.1	L28712	Zea mays heat shock protein 26. HSP26. plastid-localized low molecular weight hsp.
BAA29066.1	AB006043	Nicotiana sylvestris heat shock protein 26. hsp26. plastid-localized small heat shock protein.
BAA29067.1	AB006044	Nicotiana tomentosiformis heat shock protein 26. hsp26. plastid-localized small heat shock protein.
BAA29065.1	AB006041	Nicotiana tabacum heat shock protein 26 (Type I). Nthsp26a. plastid-localized small heat shock protein 26.
AAC01570.1	AF019144	Agrostis stolonifera var. palustris low molecular weight heat shock protein.
AAD30452.1	AF123255	Lycopersicon esculentum 17.7 kD class I small heat shock protein. HSP17.7.
CAA39603.1	X56138	Lycopersicon esculentum small heat shock protein (class I).
AAD30453.1	AF123256	Lycopersicon esculentum 17.8 kD class I small heat shock protein. HSP17.8.
AAD30454.1	AF123257	Lycopersicon esculentum 17.6 kD class I small heat shock protein. HSP17.6.
AAD49336.1	AF166277	Nicotiana tabacum low molecular weight heat-shock protein. LHS-1. TLHS-1.
AAF34133.1	AF161179	Malus x domestica low molecular weight heat shock protein. Hsp1.
AAC39360.1	U63631	Fragaria x ananassa LMW heat shock protein.
AAA61632.1	U08601	Papaver somniferum low molecular weight heat-shock protein.
CAA08908.1	AJ009880	Castanea sativa molecular chaperone. cytosolic class I small heat-shock protein HSP17.5. hsp17.5.
AAA33975.1	M11395	Glycine max small heat shock protein.
CAA63570.1	X92983	Pseudotsuga menziesii low molecular weight heat-shock protein.
AAB03893.1	M11318	Glycine max 17.5 kd heat shock protein Gmhsp17.6L.
CAA25578.1	X01104	Glycine max heat shock protein 6871 (aa 1-153).
AAB72109.1	AF022217	Brassica rapa low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.
CAA46641.1	X65725	Zea mays heat shock protein 17.2. Zmhsp 17.2. Class I low molecular weight heat shock protein.
CAB08441.1	Z95153	Helianthus annuus 17.6 kD class I small heat-shock protein HSP17.6. Ha hsp17.6.

AAA33974.1	M11317	Glycine max 17.6 kd heat shock protein Gmhsp17.6L.
SEQ ID NO: 588		
AAA32913.1	M32885	Persea americana cytochrome P-450LXXIA1 (cyp71A1).
AAA19701.1	L24438	Thlaspi arvense cytochrome P450.
AAC39318.1 AF029858 Sorghum bicolor second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldioxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.		
BAB40323.1	AB037244	Asparagus officinalis cytochrome P450. ASPI-1.
BAB40324.1	AB037245	Asparagus officinalis cytochrome P450. ASPI-2.
AAB94589.1	AF022460	Glycine max CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
AAB94584.1	AF022157	Glycine max capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
AAB61965.1	U48435	Solanum chacoense putative cytochrome P450.
AAF27282.1	AF122821	Capsicum annuum cytochrome P450. PepCYP.
CAB56503.1	AJ238612	Catharanthus roseus cytochrome P450.
AAD47832.1	AF166332	Nicotiana tabacum cytochrome P450.
AAB94588.1	AF022459	Glycine max CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAB61964.1	U48434	Solanum chacoense putative cytochrome P450.
CAA71517.1	Y10493	Glycine max putative cytochrome P450.
CAA50645.1	X71654	Solanum melongena P450 hydroxylase.
BAA03635.1	D14990	Solanum melongena Cytochrome P-450EG4.

CAA50312.1 X70981 Solanum melongena
P450 hydroxylase. CYPEG2.

CAA71514.1 Y10490 Glycine max
putative cytochrome P450.

AAB69644.1 AF000403 Lotus japonicus
putative cytochrome P450. LjNP450.

CAA70576.1 Y09424 Nepeta racemosa
cytochrome P450. CYP71A6.

AAD44151.1 AF124816 Mentha x piperita
cytochrome p450 isoform PM17.

AAK38084.1 AF321860 Lolium rigidum
putative cytochrome P450.

CAA83941.1 Z33875 Mentha x piperita
cytochrome P-450 oxidase.

AAK38083.1 AF321859 Lolium rigidum
putative cytochrome P450.

AAD44152.1 AF124817 Mentha x piperita
cytochrome p450 isoform PM2.

BAB39252.1 AP002968 Oryza sativa
putative cytochrome P450. P0416G11.1.

AAD44150.1 AF124815 Mentha spicata
cytochrome p450.

AAK38087.1 AF321863 Lolium rigidum
putative cytochrome P450.

AAK38082.1 AF321858 Lolium rigidum
putative cytochrome P450.

CAA57423.1 X81829 Zea mays
cytochrome P450. CYP71C2. family CYP71, subfamily CYP71C.

CAA72208.1 Y11404 Zea mays
cytochrome p450. cyp71c2.

CAC27827.1 AJ295719 Catharanthus roseus
geraniol hydroxylase. cytochrome P450. cyp71.

AAG44132.1 AF218296 Pisum sativum
cytochrome P450. P450 isolog.

AAK38088.1 AF321864 Lolium rigidum
putative cytochrome P450.

AAG14963.1 AF214009 Brassica napus
cytochrome p450-dependent monooxygenase. BNF5H3.

CAA57424.2 X81830 Zea mays
cytochrome P450. CYP71C3. family CYP71, subfamily CYP71C.

CAA72207.1 Y11403 Zea mays
cytochrome p450. cyp71c3.

AAG14962.1 AF214008 *Brassica napus*
cytochrome p450-dependent monooxygenase. BNF5H2.

AAG14961.1 AF214007 *Brassica napus*
cytochrome p450-dependent monooxygenase. BNF5H1.

BAA12159.1 D83968 *Glycine max*
Cytochrome P-450 (CYP93A1).

BAB40322.1 AB036772 *Triticum aestivum*
cytochrome P450. N-1.

SEQ ID NO: 593

BAA09645.1 D63331 *Nicotiana tabacum*
Indole-3-acetonitrile hydrolysis. nitrilase. TNIT4. Indole-3-acetonitrile hydolysis,indole-3-acetic acid biosynthesis.

BAA11770.1 D83078 *Nicotiana tabacum*
indole-3-acetonitrile hydolysis. nitrilase. TNIT4B. indole-3-acetonitrile hydlysis, indole-3-aceticacid biosynthesis.

BAA77679.1 AB027054 *Oryza sativa*
nitrilase-like protein. ONIT4.

SEQ ID NO: 595

AAG01147.1 AF283816 *Pinus taeda*
calreticulin. calcium-binding protein.

CAA05161.1 AJ002057 *Beta vulgaris*
calreticulin.

AAB71419.1 U74630 *Ricinus communis*
calreticulin.

AAB71420.1 U74631 *Ricinus communis*
endoplasmic reticulum calcium binding protein. calreticulin.

CAA95999.1 Z71395 *Nicotiana plumbaginifolia*
ER Ca²⁺ binding protein. calreticulin. cal1.

AAD17490.1 AF052040 *Berberis stolonifera*
possible molecular chaperon. calreticulin. calcium binding protein of the endoplasmic reticulum.

AAD32207.1 AF134733 *Prunus armeniaca*
calcium-binding protein calreticulin.

CAA61939.1 X89813 *Zea mays*
Calreticulin precursor.

AAA32948.1 L27348 *Hordeum vulgare*
calcium binding protein. calreticulin. CRH1.

AAA32949.1 L27349 *Hordeum vulgare*
calcium binding protein. calreticulin. CRH2.

AAF01470.1 AF190454 *Zea mays*
calreticulin. CRT. calcium binding protien.

CAB54526.1 AJ000765 *Chlamydomonas reinhardtii*
calreticulin.

AAB70919.1 AF019376 *Brassica napus*
calreticulin. Crt1. calcium binding protein; similar to *A. thaliana* calreticulin encoded by GenBank Accession Number U66343.

BAA85118.1 AB018243 *Solanum melongena*
calreticulin-like protein. EEF22.

CAA54975.1 X78057 *Zea mays*
calreticulin. CRH.

CAA57914.1 X82578 *Parthenium argentatum*
calreticulin. 111R.

AAK15502.1 AF325720 *Pennisetum ciliare*
calreticulin-like protein. Pcp4.

BAA77025.1 AB026251 *Lithospermum erythrorhizon*
calreticulin.

SEQ ID NO: 596

BAA12206.1 D84061 *Spinacia oleracea*
phosphoserine aminotransferase.

SEQ ID NO: 597

AAF73124.1 AF148534 *Lycopersicon esculentum*
whitefly-induced gp91-phox. Wf1. mammalian gp91-phox homolog; respiratory burst oxidase homolog; putative NADPH oxidase; similar to neutrophil NADPH oxidase gp91-phox subunit; similar to *Arabidopsis thaliana* Rboh and *Oryza sativa* Rboh; similar to *Caenorhabditis elegans* PhoX-like proteins.

AAF73104.1 AF147783 *Lycopersicon esculentum*
whitefly-induced gp91-phox. Wf1. mammalian gp91-phox homolog; respiratory burst oxidase homolog; putative NADPH oxidase; similar to neutrophil NADPH oxidase gp1-phox subunit; similar to *Arabidopsis thaliana* Rboh and *Oryza sativa* Rboh.

AAD25300.1 AF088276 *Lycopersicon esculentum*
NADPH oxidase. RBOH1. gp91; phox homolog.

AAB87790.1 AF015302 *Oryza sativa*
RbohAOsp. putative NADPH oxidase; intrinsic plasma membrane protein; similar to the neutrophil NADPH oxidase gp91phox subunit; contains RanGAP1 domain; similar to *O. sativa* NAD(P)H oxidase sequence with GenBank Accession Number X93301.

CAA63704.1 X93301 *Oryza sativa*
NAD(P)H oxidase. rbohA.

AAD24966.1 AF109150 *Lycopersicon esculentum*
NADPH oxidase. gp91; phox homolog.

AAD25225.1 AF088279 *Potamogeton crispus*
NADPH oxidase. RBOH1. gp91; phox homolog.

SEQ ID NO: 599

CAC21424.1 AJ278332 *Lycopersicon esculentum*
involved in octadecanoid biosynthesis. 12-oxophytodienoate reductase 3. opr3.

BAB40340.1 AB044940 *Pisum sativum*
12-oxophytodienoic acid 10, 11-reductase. OPDAR.

CAB43506.1	AJ242551	<i>Lycopersicon esculentum</i> involved in jasmonic acid biosynthesis. 12-oxophytodienoate reductase. opr.
CAC21423.1	AJ278331	<i>Lycopersicon esculentum</i> involved in octadecanoid biosynthesis. putative 12-oxophytodienoate reductase 2. opr2.
CAB97122.1	AJ297421	<i>Daucus carota</i> oxidoreductase. putative 12-oxophytodienoate reductase. opr2.
SEQ ID NO: 602		
AAB37246.1	U58971	<i>Nicotiana tabacum</i> calmodulin-binding protein. TCB60.
SEQ ID NO: 603		
AAK15006.1	AF233433	<i>Brassica napus</i> arginase. similar to <i>Arabidopsis thaliana</i> and <i>Glycine max</i> arginase.
AAK07744.1	AF130440	<i>Pinus taeda</i> converts L-arginine to L-ornithine and urea. arginase. ARS20. L-arginine amidinohydrolase.
AAC04613.1	AF035671	<i>Glycine max</i> hydrolysis of L-Arg to L-Orn and urea. arginase. pAG1. L-Arg amidinohydrolase.
SEQ ID NO: 605		
CAA81210.1	Z26251	<i>Helianthus tuberosus</i> Catalyzes the reduction of cytochrome P450 in microsomes. NADPH-ferredoxin reductase.
AAB02721.1	U58629	<i>Helianthus tuberosus</i> NADPH-ferredoxin oxidoreductase. HTR2. NADPH-cytochrome P450 reductase isoform.
CAC27143.1	AJ132538	<i>Picea abies</i> NADPH-cytochrome P450 reductase.
AAA79131.1	U10545	<i>Chlamydomonas reinhardtii</i> ferredoxin-NADP+ reductase. fnr.
CAA55406.1	X78851	<i>Chlamydomonas reinhardtii</i> ferredoxin NADP reductase.
AAB40978.1	U22328	<i>Volvox carteri</i> ferredoxin-NADP+ reductase. fnr. FNR.
AAA33029.1	M25528	<i>Mesembryanthemum crystallinum</i> ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1).
CAA30978.1	X12446	<i>Pisum sativum</i> ferredoxin-NADH+ reductase preprotein (AA -52 to 308).
BAA13417.1	D87547	<i>Oryza sativa</i> ferredoxin-NADP+ oxidoreductase.
AAA21758.1	U14956	<i>Vicia faba</i> photosynthetic electron transport. ferredoxin NADP+ reductase precursor. fnr.
AAA34029.1	M86349	<i>Spinacia oleracea</i> ferredoxin-NADP oxidoreductase. precursor protein.
CAB71293.1	AJ250378	<i>Capsicum annuum</i> chloroplast ferredoxin-NADP+ oxidoreductase precursor. fnr.

CAA74359.1	Y14032	Nicotiana tabacum ferredoxin-NADP(+) reductase. fnr.
BAA88236.1	AB035644	Zea mays NADP+ oxidoreductase. ferredoxin. L-FNRI.
BAA88237.1	AB035645	Zea mays NADP+ oxidoreductase. ferredoxin. L-FNRII.
BAA20365.1	AB004307	Nicotiana tabacum ferredoxin-NADP oxidoreductase.
BAA07479.1	D38445	Oryza sativa root ferredoxin-NADP+ reductase. root FNR. nitrate assimilation pathway.
BAA02248.1	D12815	Oryza sativa ferredoxin-NADP+ reductase enzyme.
BAA04232.1	D17410	Oryza sativa ferredoxin-NADP+ reductase.
BAA90642.1	AP001129	Oryza sativa ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; Similar to Oryza sativa, ferredoxin-NADP+ reductase. (D17790).
BAA85425.1	AP000616	Oryza sativa ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790).
BAA04616.1	D17790	Oryza sativa ferredoxin-NADP+ reductase.
AAB40034.1	U10418	Zea mays ferredoxin-NADP reductase precursor.
CAA67796.1	X99419	Pisum sativum ferredoxin NADP oxidoreductase.
AAK09367.1	AF321525	Pisum sativum ferredoxin-NADP+ reductase. FNR.
AAK09370.1	AF321528	Pisum sativum ferredoxin-NADP+ reductase. FNR.
AAK09369.1	AF321527	Pisum sativum ferredoxin-NADP+ reductase. FNR.
AAK09368.1	AF321526	Pisum sativum ferredoxin-NADP+ reductase. FNR.
SEQ ID NO: 606		
BAA82107.1	AB022693	Nicotiana tabacum transcription factor. NtWRKY1.
AAC31956.1	AF080595	Pimpinella brachycarpa zinc finger protein. ZFP1. WRKY1.
AAC49527.1	U48831	Petroselinum crispum WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.

AAD55974.1	AF121353	Petroselinum crispum zinc-finger type transcription factor WRKY1. WRKY1.
BAA77383.1	AB020590	Nicotiana tabacum transcription factor NtWRKY2.
AAD32677.1	AF140554	Avena sativa DNA-binding protein WRKY1. wrky1. putative transcription factor.
CAA88326.1	Z48429	Avena fatua binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
BAA86031.1	AB026890	Nicotiana tabacum transcription factor NtWRKY4.
AAD16139.1	AF096299	Nicotiana tabacum DNA-binding protein 2. WRKY2. transcription factor.
AAC37515.1	L44134	Cucumis sativus SPF1-like DNA-binding protein.
AAF23898.1	AF193802	Oryza sativa zinc finger transcription factor WRKY1.
AAK16171.1	AC079887	Oryza sativa putative DNA-binding protein. OSJNBa0040E01.10.
AAC49529.1	U58540	Petroselinum crispum WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
AAD16138.1	AF096298	Nicotiana tabacum DNA-binding protein 1. WRKY1. transcription factor.
BAB19096.1	AP002839	Oryza sativa putative DNA-binding protein homolog. P0688A04.2.
BAB19075.1	AP002744	Oryza sativa putative DNA-binding protein homolog. P0006C01.17.
AAK16170.1	AC079887	Oryza sativa putative DNA binding protein. OSJNBa0040E01.4.
CAB97004.1	AJ278507	Solanum tuberosum putative transcription factor. WRKY DNA binding protein. WRKY1.
BAB18313.1	AP002865	Oryza sativa putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
AAD38283.1	AC007789	Oryza sativa putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAB40073.1	AP003074	Oryza sativa putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
AAC49528.1	U56834	Petroselinum crispum DNA-binding. WRKY3. WRKY-type DNA-binding protein.
BAB16432.1	AB041520	Nicotiana tabacum WRKY transcription factor Nt-SubD48. Nt-SubD48.
BAA77358.1	AB020023	Nicotiana tabacum WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.

AAD32676.1	AF140553	<i>Avena sativa</i>
DNA-binding protein WRKY3. wrky3. putative transcription factor.		
CAA88331.1	Z48431	<i>Avena fatua</i>
binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.		
AAG35658.1	AF204925	<i>Petroselinum crispum</i>
transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.		
AAG46150.1	AC018727	<i>Oryza sativa</i>
putative DNA-binding protein. OSJNBa0056G17.18.		
AAD27591.1	AF121354	<i>Petroselinum crispum</i>
binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.		
AAG35659.1	AF204926	<i>Petroselinum crispum</i>
transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.		
CAB66338.1	AJ279697	<i>Betula pendula</i>
wrky-type DNA binding protein. wrky.		
AAF61864.1	AF193771	<i>Nicotiana tabacum</i>
DNA-binding protein 4. WRKY4. transcription factor.		
AAF61863.1	AF193770	<i>Nicotiana tabacum</i>
DNA-binding protein 3. WRKY3. transcription factor.		
SEQ ID NO: 608		
BAA87853.1	AP000816	<i>Oryza sativa</i>
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).		
AAK21965.1	AY028699	<i>Brassica napus</i>
receptor protein kinase PERK1.		
BAB21240.1	AP002953	<i>Oryza sativa</i>
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).		
BAB19337.1	AP003044	<i>Oryza sativa</i>
putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).		
BAA92836.1	AB032473	<i>Brassica oleracea</i>
S18 S-locus receptor kinase. SRK18.		
AAB61708.1	U93048	<i>Daucus carota</i>
somatic embryogenesis receptor-like kinase. SERK.		
BAA23676.1	AB000970	<i>Brassica rapa</i>
receptor kinase 1. BcRK1.		
AAK00425.1	AC069324	<i>Oryza sativa</i>
Putative protein kinase. OSJNBa0071K19.11.		
BAB39873.1	AP002882	<i>Oryza sativa</i>
putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).		
AAD21872.1	AF078082	<i>Phaseolus vulgaris</i>
receptor-like protein kinase homolog RK20-1.		

CAB41878.1	Y18259	Brassica oleracea
<u>SRK5 protein. SRK5. receptor-like kinase.</u>		
AAA62232.1	U00443	Brassica napus
<u>S-receptor kinase. protein contains an immunoglobulin-like domain.</u>		
AAA33000.1	M76647	Brassica oleracea
<u>receptor protein kinase. SKR6.</u>		
AAG59657.1	AC084319	Oryza sativa
<u>putative protein kinase. OSJNBa0004B24.20.</u>		
CAB41879.1	Y18260	Brassica oleracea
<u>SRK15 protein. SRK15. receptor-like kinase.</u>		
CAA73134.1	Y12531	Brassica oleracea
<u>serine/threonine kinase. BRLK.</u>		
BAB16871.1	AP002537	Oryza sativa
<u>putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).</u>		
BAB18292.1	AP002860	Oryza sativa
<u>putative receptor-like protein kinase. P0409B08.19.</u>		
BAA06285.1	D30049	Brassica rapa
<u>S-receptor kinase SRK9.</u>		
BAA21132.1	D88193	Brassica rapa
<u>S-receptor kinase. SRK9 (B.c).</u>		
CAB89179.1	AJ245479	Brassica napus subsp. napus
<u>ser /thr kinase. S-locus receptor kinase. srk.</u>		
AAA33008.1	M97667	Brassica napus
<u>serine/threonine kinase receptor.</u>		
CAA67145.1	X98520	Brassica oleracea
<u>receptor-like kinase. SFR2.</u>		
CAA73133.1	Y12530	Brassica oleracea
<u>serine /threonine kinase. ARLK.</u>		
AAF66615.1	AF142596	Nicotiana tabacum
<u>LRK receptor-like protein kinase.</u>		
AAF76314.1	AF220603	Lycopersicon esculentum
<u>Fen kinase. Lescfen.</u>		
AAK11568.1	AF318492	Lycopersicon hirsutum
<u>Pto-like protein kinase B. LhirPtoB.</u>		
CAA74662.1	Y14286	Brassica oleracea
<u>SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.</u>		
AAB47424.1	U59317	Lycopersicon pimpinellifolium
<u>serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.</u>		
AAB47422.1	U59318	Lycopersicon esculentum
<u>serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.</u>		

AAC48932.1	U13923	Lycopersicon pimpinellifolium Fen. putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.
AAF76307.1	AF220602	Lycopersicon pimpinellifolium Fen kinase.
BAA07576.1	D38563	Brassica rapa receptor protein kinase SRK8.
AAG16628.1	AY007545	Brassica napus protein serine/threonine kinase BNK1.
CAA97692.1	Z73295	Catharanthus roseus receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
CAA79355.1	Z18921	Brassica oleracea S-receptor kinase-like protein.
AAB93834.1	U82481	Zea mays KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
BAA92837.1	AB032474	Brassica oleracea S60 S-locus receptor kinase. SRK60.
AAA33915.1	L27821	Oryza sativa receptor type serine/threonine kinase. protein kinase.
SEQ ID NO: 610		
BAB17348.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.32.
BAB17345.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.29.
BAB17126.1	AP002867	Oryza sativa putative receptor kinase. P0463F06.16.
BAB39451.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.24.
BAB17342.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.26.
AAC27489.1	AF077130	Oryza sativa receptor-like protein kinase.
AAF78018.1	AF238474	Oryza sativa receptor-like kinase. RLG16. protein kinase.
AAC02535.1	AF044260	Oryza sativa receptor serine/threonine kinase. protein kinase.
BAB39435.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.2.
AAD46917.1	AF164021	Oryza sativa receptor kinase.

BAB39438.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.7.
BAB17339.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.23.
AAC49629.1	U51330	Triticum aestivum rust resistance kinase Lr10. LRK10.
BAB17321.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.1.
BAB17129.1	AP002867	Oryza sativa putative receptor kinase. P0463F06.20.
AAF68398.1	AF237568	Oryza sativa receptor-like protein kinase. RLG2.
BAB17331.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.12.
BAB17139.1	AP002867	Oryza sativa putative receptor kinase. P0463F06.31.
AAC01746.1	AF044489	Oryza sativa receptor-like protein kinase. drpk1.
AAF78016.1	AF238472	Oryza sativa receptor-like kinase. RLG15. protein kinase.
BAB39441.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.11.
BAB17116.1	AP002867	Oryza sativa putative receptor kinase. P0463F06.3.
AAF78044.1	AF248493	Oryza sativa receptor-like kinase. RLG18. protein kinase.
AAD44029.1	AF085164	Hordeum vulgare receptor-like kinase LRK10.
BAB17332.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.13. contains ESTs D47575(S13157),AU032665(S13157).
BAB17347.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.31. contains ESTs D47575(S13157),AU032665(S13157).
BAB17344.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.28. contains ESTs D47575(S13157),AU032665(S13157).
BAB17337.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.21. contains ESTs D47575(S13157),AU032665(S13157).
BAB17335.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.17. contains ESTs D47575(S13157),AU032665(S13157).
BAB17115.1	AP002867	Oryza sativa putative receptor kinase. P0463F06.2.
BAB39440.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.10.

BAB39437.1 AP003338 Oryza sativa
receptor-like kinase. OJ1212_B09.6.

AAF78019.1 AF238475 Oryza sativa
receptor-like kinase. RLG17. protein kinase.

BAB17127.1 AP002867 Oryza sativa
putative receptor kinase. P0463F06.17.

AAD46916.1 AF164020 Oryza sativa
receptor kinase.

AAF78021.1 AF238477 Oryza sativa
receptor-like kinase. RLG5. protein kinase.

AAD46417.1 AF100767 Oryza sativa
receptor-like kinase. 8ARK3. similar to wheat ARK1AS.

AAD46415.1 AF100765 Oryza sativa
receptor-like kinase. 8ARK1. similar to wheat ARK1AS.

BAB17128.1 AP002867 Oryza sativa
putative receptor kinase. P0463F06.18.

AAF68400.1 AF237570 Oryza sativa
receptor-like protein kinase. RLG3.

BAB17323.1 AP002747 Oryza sativa
putative receptor kinase. P0698G03.3.

BAB17131.1 AP002867 Oryza sativa
putative receptor kinase. P0463F06.22.

AAF68397.1 AF237567 Oryza sativa
receptor-like protein kinase. RLG1.

AAF78015.1 AF238471 Oryza sativa
receptor-like kinase. RLG10. protein kinase.

AAD43962.1 U78762 Triticum aestivum
receptor-like kinase ARK1AS. ARK1AS.

SEQ ID NO: 611

BAA78764.1 AB023482 Oryza sativa
ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to *Arabidopsis thaliana* APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).

AAK11674.1 AF339747 Lophopyrum elongatum
protein kinase. ESI47.

AAF43496.1 AF131222 Lophopyrum elongatum
protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.

AAG16628.1 AY007545 Brassica napus
protein serine/threonine kinase BNK1.

BAA94509.1 AB041503 Populus nigra
protein kinase 1. PnPK1.

BAA94510.1 AB041504 Populus nigra
protein kinase 2. PnPK2.

BAB07999.1	AP002525	Oryza sativa putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB03429.1	AP002817	Oryza sativa EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
CAB51834.1	00069	Oryza sativa l1332.5. contains eukaryotic protein kinase domain PF.
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK11567.1	AF318491	Lycopersicon hirsutum Pto-like protein kinase F. LhirPtoF.
BAA90808.1	AP001168	Oryza sativa Similar to putative receptor-like protein kinase (AL035679).
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
AAC48932.1	U13923	Lycopersicon pimpinellifolium Fen. putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.
AAB47424.1	U59317	Lycopersicon pimpinellifolium serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.
AAF76307.1	AF220602	Lycopersicon pimpinellifolium Fen kinase.
AAK11566.1	AF318490	Lycopersicon hirsutum Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
AAG03090.1	AC073405	Oryza sativa Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAF76314.1	AF220603	Lycopersicon esculentum Fen kinase. Lescfen.

AAB47421.1 U59316 *Lycopersicon esculentum*
serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.

AAF76313.1 AF220603 *Lycopersicon esculentum*
Pto kinase. LescPth5.

AAB47422.1 U59318 *Lycopersicon esculentum*
serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.

AAG59657.1 AC084319 *Oryza sativa*
putative protein kinase. OSJNBa0004B24.20.

AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*
Pto kinase.

AAB47423.1 U59315 *Lycopersicon pimpinellifolium*
serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.

AAC48914.1 U02271 *Lycopersicon pimpinellifolium*
protein kinase.

AAK11568.1 AF318492 *Lycopersicon hirsutum*
Pto-like protein kinase B. LhirPtoB.

BAB21241.1 AP002953 *Oryza sativa*
Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721), D48017(S13927).

AAC27894.1 AF023164 *Zea mays*
leucine-rich repeat transmembrane protein kinase 1. ltk1.

AAF91337.1 AF249318 *Glycine max*
Pt1 kinase-like protein. Pt1b. protein kinase.

AAC61805.1 U28007 *Lycopersicon esculentum*
serine/threonine protein kinase. Pto kinase interactor 1. Pt1. Pt1 kinase.

CAA97692.1 Z73295 *Catharanthus roseus*
receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

AAF91336.1 AF249317 *Glycine max*
Pt1 kinase-like protein. Pt1a. protein kinase.

AAF66615.1 AF142596 *Nicotiana tabacum*
LRR receptor-like protein kinase.

AAB61708.1 U93048 *Daucus carota*
somatic embryogenesis receptor-like kinase. SERK.

AAK11569.1 AF318493 *Lycopersicon hirsutum*
Pto-like protein kinase D. LhirPtoD.

BAA92221.1 AP001278 *Oryza sativa*
Similar to *Arabidopsis thaliana* chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).

BAA87852.1 AP000816 *Oryza sativa*
Similar to putative Ser/Thr protein kinase. (AC004218).

AAC27895.1 AF023165 *Zea mays*
 leucine-rich repeat transmembrane protein kinase 2. ltk2.

SEQ ID NO: 612

CAA54613.1 X77463 *Manihot esculenta*
 UTP-glucose glucosyltransferase. CGT6.

CAA54609.1 X77459 *Manihot esculenta*
 UTP-glucose glucosyltransferase. CGT1.

CAA54611.1 X77461 *Manihot esculenta*
 UTP-glucose glucosyltransferase. CGT2.

CAA54612.1 X77462 *Manihot esculenta*
 UTP-glucose glucosyltransferase. CGT5.

BAB17182.1 AP002843 *Oryza sativa*
 putative UTP-glucose glucosyltransferase. P0407B12.19.

BAB17176.1 AP002843 *Oryza sativa*
 putative UTP-glucose glucosyltransferase. P0407B12.13.

CAB56231.1 Y18871 *Dorotheanthus bellidiformis*
 betanidin-5-O-glucosyltransferase.

BAA83484.1 AB031274 *Scutellaria baicalensis*
 UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

AAB36653.1 U32644 *Nicotiana tabacum*
 immediate-early salicylate-induced glucosyltransferase. IS5a.

AAK28303.1 AF346431 *Nicotiana tabacum*
 phenylpropanoid:glucosyltransferase 1. tog1. glucosyltransferase.

CAA59450.1 X85138 *Lycopersicon esculentum*
 twi1. homologous to glucosyltransferases.

AAB36652.1 U32643 *Nicotiana tabacum*
 immediate-early salicylate-induced glucosyltransferase. IS10a.

AAK28304.1 AF346432 *Nicotiana tabacum*
 phenylpropanoid:glucosyltransferase 2. tog2. glucosyltransferase.

BAA89009.1 AB027455 *Petunia x hybrida*
 anthocyanin 5-O-glucosyltransferase. PH1.

AAG25643.1 AF303396 *Phaseolus vulgaris*
 UDP-glucosyltransferase HRA25. putative; defense associated.

AAF61647.1 AF190634 *Nicotiana tabacum*
 UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA93039.1 AB033758 *Citrus unshiu*
 limonoid UDP-glucosyltransferase. LGTase.

AAB48444.1 U82367 *Solanum tuberosum*
 UDP-glucose glucosyltransferase.

AAD21086.1 AF127218 *Forsythia x intermedia*
 adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.

AAK16175.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.15.
CAC09351.1	AL442007	Oryza sativa putative glucosyltransferase. H0212B02.7.
AAD04166.1	AF101972	Phaseolus lunatus catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
AAF17077.1	AF199453	Sorghum bicolor UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
BAA12737.1	D85186	Gentiana triflora UDP-glucose:flavonoid-3-glucosyltransferase.
BAB07962.1	AP002524	Oryza sativa putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
BAA36421.1	AB013596	Perilla frutescens UDP-glucose:anthocysnin 5-O-glucosyltransferase. PF3R4.
CAA54610.1	X77460	Manihot esculenta UTP-glucose glucosyltransferase. CGT4.
AAF98390.1	AF287143	Brassica napus catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
BAA36423.1	AB013598	Verbena x hybrida UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
CAA30760.1	X07937	Zea mays UDPGlucose flavonoid glycosyl transferase. Bz-W22.
CAA30761.1	X07940	Zea mays UDPGlucose flavonoid glycosyl-transferase. Bz-McC.
CAA31855.1	X13500	Zea mays UDPGlucose:flavonol 3-O-glucosyltransferase.
BAA19659.1	AB002818	Perilla frutescens flavonoid 3-O-glucosyltransferase. UDP glucose.
BAA89008.1	AB027454	Petunia x hybrida anthocyanidin 3-O-glucosyltransferase. PGT8.
AAK16172.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.14.
SEQ ID NO: 613		
CAA54609.1	X77459	Manihot esculenta UTP-glucose glucosyltransferase. CGT1.
CAA54613.1	X77463	Manihot esculenta UTP-glucose glucosyltransferase. CGT6.

CAA54611.1	X77461	<i>Manihot esculenta</i>
		UTP-glucose glucosyltransferase. CGT2.
CAA54612.1	X77462	<i>Manihot esculenta</i>
		UTP-glucose glucosyltransferase. CGT5.
BAB17182.1	AP002843	<i>Oryza sativa</i>
		putative UTP-glucose glucosyltransferase. P0407B12.19.
BAB17176.1	AP002843	<i>Oryza sativa</i>
		putative UTP-glucose glucosyltransferase. P0407B12.13.
CAB56231.1	Y18871	<i>Dorotheanthus bellidiformis</i>
		betanidin-5-O-glucosyltransferase.
AAB36653.1	U32644	<i>Nicotiana tabacum</i>
		immediate-early salicylate-induced glucosyltransferase. IS5a.
AAK28303.1	AF346431	<i>Nicotiana tabacum</i>
		phenylpropanoid:glucosyltransferase 1. tog1. glucosyltransferase.
AAB36652.1	U32643	<i>Nicotiana tabacum</i>
		immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	<i>Nicotiana tabacum</i>
		phenylpropanoid:glucosyltransferase 2. tog2. glucosyltransferase.
CAA59450.1	X85138	<i>Lycopersicon esculentum</i>
		tw1. homologous to glucosyltransferases.
BAA83484.1	AB031274	<i>Scutellaria baicalensis</i>
		UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAF61647.1	AF190634	<i>Nicotiana tabacum</i>
		UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA93039.1	AB033758	<i>Citrus unshiu</i>
		limonoid UDP-glucosyltransferase. LGTase.
AAB48444.1	U82367	<i>Solanum tuberosum</i>
		UDP-glucose glucosyltransferase.
BAA89009.1	AB027455	<i>Petunia x hybrida</i>
		anthocyanin 5-O-glucosyltransferase. PH1.
BAA36421.1	AB013596	<i>Perilla frutescens</i>
		UDP-glucose:anthocysnin 5-O-glucosyltransferase. PF3R4.
CAC09351.1	AL442007	<i>Oryza sativa</i>
		putative glucosyltransferase. H0212B02.7.
BAA12737.1	D85186	<i>Gentiana triflora</i>
		UDP-glucose:flavonoid-3-glucosyltransferase.
AAG25643.1	AF303396	<i>Phaseolus vulgaris</i>
		UDP-glucosyltransferase HRA25. putative; defense associated.
AAD04166.1	AF101972	<i>Phaseolus lunatus</i>
		catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

CAA54610.1	X77460	<i>Manihot esculenta</i>
		<u>UTP-glucose glucosyltransferase. CGT4.</u>
AAF98390.1	AF287143	<i>Brassica napus</i>
		catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
AAK16172.1	AC079887	<i>Oryza sativa</i>
		<u>putative glucosyltransferase. OSJNBa0040E01.14.</u>
BAA36423.1	AB013598	<i>Verbena x hybrida</i>
		<u>UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.</u>
AAD21086.1	AF127218	<i>Forsythia x intermedia</i>
		adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
AAF17077.1	AF199453	<i>Sorghum bicolor</i>
		<u>UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.</u>
AAK16175.1	AC079887	<i>Oryza sativa</i>
		<u>putative glucosyltransferase. OSJNBa0040E01.15.</u>
BAB07962.1	AP002524	<i>Oryza sativa</i>
		putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
CAA31855.1	X13500	<i>Zea mays</i>
		<u>UDPGlucose:flavonol 3-O-glucosyltransferase.</u>
BAA36422.1	AB013597	<i>Perilla frutescens</i>
		<u>UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.</u>
BAA89008.1	AB027454	<i>Petunia x hybrida</i>
		<u>anthocyanidin 3-O-glucosyltransferase. PGT8.</u>
SEQ ID NO: 614		
AAD21872.1	AF078082	<i>Phaseolus vulgaris</i>
		<u>receptor-like protein kinase homolog RK20-1.</u>
CAA73134.1	Y12531	<i>Brassica oleracea</i>
		<u>serine/threonine kinase. BRLK.</u>
AAB93834.1	U82481	<i>Zea mays</i>
		KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAA33008.1	M97667	<i>Brassica napus</i>
		<u>serine/threonine kinase receptor.</u>
CAB89179.1	AJ245479	<i>Brassica napus subsp. napus</i>
		<u>ser /thr kinase. S-locus receptor kinase. srk.</u>
AAA33000.1	M76647	<i>Brassica oleracea</i>
		<u>receptor protein kinase. SKR6.</u>
BAA23676.1	AB000970	<i>Brassica rapa</i>
		<u>receptor kinase 1. BcRK1.</u>

BAA06285.1	D30049	Brassica rapa S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa S-receptor kinase. SRK9 (B.c.).
CAA74661.1	Y14285	Brassica oleracea SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
BAA92837.1	AB032474	Brassica oleracea S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa receptor protein kinase SRK12.
BAA07576.1	D38563	Brassica rapa receptor protein kinase SRK8.
CAA73133.1	Y12530	Brassica oleracea serine /threonine kinase. ARLK.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
CAA79355.1	Z18921	Brassica oleracea S-receptor kinase-like protein.
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
CAA74662.1	Y14286	Brassica oleracea SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAB21001.1	AB054061	Brassica rapa S locus receptor kinase. SRK22.
AAA62232.1	U00443	Brassica napus S-receptor kinase. protein contains an immunoglobulin-like domain.
CAB41879.1	Y18260	Brassica oleracea SRK15 protein. SRK15. receptor-like kinase.
CAB41878.1	Y18259	Brassica oleracea SRK5 protein. SRK5. receptor-like kinase.
BAA92836.1	AB032473	Brassica oleracea S18 S-locus receptor kinase. SRK18.
BAB18292.1	AP002860	Oryza sativa putative receptor-like protein kinase. P0409B08.19.
AAD52097.1	AF088885	Nicotiana tabacum receptor-like kinase CHRK1. Chrk1.
AAA33915.1	L27821	Oryza sativa receptor type serine/threonine kinase. protein kinase.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBA0071K19.11.
BAA94529.2	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA94509.1	AB041503	Populus nigra protein kinase 1. PnPK1.
BAA94510.1	AB041504	Populus nigra protein kinase 2. PnPK2.
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAG03090.1	AC073405	Oryza sativa Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAA94518.1	AP001800	Oryza sativa Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAB07904.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.12.
SEQ ID NO: 619		
CAA72092.1	Y11209	Nicotiana tabacum protein disulfide-isomerase precursor. PDI.
AAG13988.1	AF298829	Prunus avium putative protein disulfide-isomerase. PDI.
AAD02069.1	AF036939	Chlamydomonas reinhardtii redox-regulator of 5'UTR psbA mRNA binding complex and translation. protein disulfide isomerase. localized to ER and chloroplast.
AAC49896.1	AF027727	Chlamydomonas reinhardtii involved in the redox-regulated binding of chloroplast poly(A)-binding protein to the 5'-UTR of psbA mRNA; regulates chloroplast translational activation. protein disulfide isomerase RB60. PDI.
AAD55566.1	AF110784	Volvox carteri f. nagariensis protein disulfide isomerase precursor. pdi.
AAB08519.1	L39014	Zea mays protein disulfide isomerase. pdi. putative.

AAA70344.1 L33250 *Hordeum vulgare*
catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.

AAA70345.1 L33251 *Hordeum vulgare*
catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.

CAC21230.1 AJ277379 *Triticum turgidum* subsp. *durum*
catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.

AAA19660.1 U11496 *Triticum aestivum*
protein disulfide isomerase. PDI.

CAC21231.1 AJ277380 *Triticum turgidum* subsp. *durum*
catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.

CAC21229.1 AJ277378 *Triticum turgidum* subsp. *durum*
catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.

CAC21228.1 AJ277377 *Triticum turgidum* subsp. *durum*
catalyzes the formation of disulfide bonds. protein disulfide isomerase. Pdi.

AAB05641.1 U41385 *Ricinus communis*
protein disulphide isomerase PDI. molecular chaperone.

CAA77575.1 Z11499 *Medicago sativa*
protein disulfide isomerase.

AAD28260.1 AF131223 *Datiscia glomerata*
protein disulfide isomerase homolog. PDI.

AAA70346.1 L33252 *Hordeum vulgare*
catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.

BAA92322.1 AB039278 *Oryza sativa*
protein disulfide isomerase. Pdi.

BAA77026.1 AB026252 *Lithospermum erythrorhizon*
disulfide-isomerase precursor.

AAC79709.1 AF093614 *Acetabularia acetabulum*
putative protein disulfide isomerase.

SEQ ID NO: 620

CAA64413.1 X94943 *Lycopersicon esculentum*
peroxidase. cevi16.

AAA32676.1 M37637 *Arachis hypogaea*
cationic peroxidase. PNC2.

BAA82307.1 AB027753 *Nicotiana tabacum*
peroxidase.

AAB67737.1 L77080 *Stylosanthes humilis*
cationic peroxidase.

AAD37429.2 AF149279 *Phaseolus vulgaris*
peroxidase 4 precursor. FBP4. secretory peroxidase.

CAA71494.1 Y10468 *Spinacia oleracea*
peroxidase. prxr7.

AAD37375.1	AF145349	Glycine max peroxidase. Prx3.
AAF63024.1	AF244921	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.
CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAB39274.1	AP002971	Oryza sativa putative peroxidase. P0537A05.2.
AAA65637.1	L13654	Lycopersicon esculentum peroxidase. TPX1.
CAA40796.1	X57564	Armoracia rusticana peroxidase. peroxidase precursor.
AAD11482.1	U51192	Glycine max peroxidase precursor. sEPa2.
CAA80502.1	Z22920	Spirodela polyrrhiza peroxidase.
BAA77387.1	AB024437	Scutellaria baicalensis peroxidase 1.
CAA59485.1	X85228	Triticum aestivum peroxidase. POX2.
BAA07663.1	D42064	Nicotiana tabacum cationic peroxidase isozyme 38K precursor.
BAA11853.1	D83225	Populus nigra peroxidase.
BAA07664.1	D42065	Nicotiana tabacum cationic peroxidase isozyme 40K precursor.
AAD37430.1	AF149280	Phaseolus vulgaris peroxidase 5 precursor. FBP5. secretory peroxidase.
AAD11481.1	U51191	Glycine max peroxidase precursor. sEPa1.
CAB94692.1	AJ242742	Ipomoea batatas Removal of H ₂ O ₂ , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
BAA03644.1	D14997	Oryza sativa peroxidase.
AAD43561.1	AF155124	Gossypium hirsutum bacterial-induced peroxidase precursor. Perx_Goshiko.
BAA06334.1	D30652	Populus kitakamiensis peroxidase.
BAA92500.1	AP001383	Oryza sativa ESTs D39300(R3292),AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).

BAA90365.1	AP001081	Oryza sativa ESTs D24550(R2151),D24265(R1609),AU031848(R2151) correspond to a region of the predicted gene. Similar to cationic peroxidase isozyme 40K precursor (D42065).
BAA89584.1	AP001073	Oryza sativa ESTs D24550(R2151),D24265(R1609),AU031848(R2151) correspond to a region of the predicted gene. Similar to cationic peroxidase isozyme 40K precursor (D42065).
AAF34416.1	AF172282	Oryza sativa putative peroxidase. DUPR11.5.
AAC49820.1	AF014469	Oryza sativa peroxidase. POX5.1. wound inducible.
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAB39281.1	AP002971	Oryza sativa putative peroxidase. P0537A05.10. contains ESTs D24657(R2329),AU082066(R2329).
BAA14144.1	D90116	Armoracia rusticana peroxidase isozyme.
AAB97734.1	AF014502	Glycine max seed coat peroxidase precursor. Ep. H2O2 oxidoreductase; class III plant peroxidase.
CAA37713.1	X53675	Triticum aestivum peroxidase.
AAC05277.1	AF049881	Linum usitatissimum peroxidase FLXPER4. PER4.
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA06335.1	D30653	Populus kitakamiensis peroxidase.
CAA39486.1	X56011	Triticum aestivum peroxidase.
BAA03911.1	D16442	Oryza sativa peroxidase.
BAA94962.1	AB042103	Asparagus officinalis peroxidase. AspPOX1.
AAC49821.1	AF014470	Oryza sativa peroxidase. POXgX9. expressed in roots.
AAD37427.1	AF149277	Phaseolus vulgaris peroxidase 1 precursor. FBP1. secretory peroxidase.
CAA76374.2	Y16776	Spinacia oleracea peroxidase. prx10.
BAA08499.1	D49551	Oryza sativa peroxidase. poxN.
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.

AAA34108.1 J02979 Nicotiana tabacum
lignin-forming peroxidase precursor (EC 1.11.1.7).

CAA62226.1 X90693 Medicago sativa
peroxidase1B. prx1B.

CAA59487.1 X85230 Triticum aestivum
peroxidase. pox4.

SEQ ID NO: 626

CAA98160.1 Z73932 Lotus japonicus
GTP-binding protein. RAB1C. rab1C.

BAA76422.1 AB024994 Cicer arietinum
rab-type small GTP-binding protein.

BAA02116.1 D12548 Pisum sativum
GTP-binding protein.

CAA69701.1 Y08425 Nicotiana plumbaginifolia
small GTP-binding protein. Rab1 subfamily.

AAA80678.1 U38464 Lycopersicon esculentum
small GTP-binding protein. LeRab1A. ; YPT1/Rab1A homolog LeRab1A.

BAA02118.1 D12550 Pisum sativum
GTP-binding protein.

AAB97115.1 U58854 Glycine max
small GTP-binding protein. sra2.

CAA51011.1 X72212 Nicotiana tabacum
ras-related GTP-binding protein. ypt2 homologue.

AAF65510.1 AF108883 Capsicum annuum
small GTP-binding protein.

AAA80680.1 U38466 Lycopersicon esculentum
small GTP-binding protein. LeRab1C. ; YPT1/Rab1A homolog LeRab1C.

CAA98161.1 Z73933 Lotus japonicus
GTP-binding protein. RAB1D. rab1D.

BAA02117.1 D12549 Pisum sativum
GTP-binding protein.

CAA98162.1 Z73934 Lotus japonicus
GTP-binding protein. RAB1E. rab1E.

AAA50159.1 L27417 Glycine max
GTP binding protein.

AAB28535.1 S66160 Oryza sativa
ric1. ras-related GTP binding protein possessing GTPase activity; This sequence comes from Fig. 1.

CAA98159.1 Z73931 Lotus japonicus
GTP-binding protein. RAB1B. rab1B.

BAA02115.1 D12547 Pisum sativum
GTP-binding protein.

CAA66447.1	X97853	Lotus japonicus GTP-binding protein. RAB1A. rab1A.
AAD10389.1	U35026	Petunia x hybrida Rab1-like small GTP-binding protein.
AAA80679.1	U38465	Lycopersicon esculentum small GTP-binding protein. LeRab1B. ; Ypt1/Rab1A homolog LeRab1B.
BAB07961.1	AP002524	Oryza sativa putative GTP-binding protein. P0406H10.17. contains ESTs D23874(R0480),AU031678(R0480).
CAA98176.1	Z73948	Lotus japonicus GTP-binding protein. RAB8E. rab8E.
CAA89021.1	Z49152	Beta vulgaris GTP-binding. small G protein.
CAA98172.1	Z73944	Lotus japonicus GTP-binding protein. RAB8A. rab8A.
CAA04701.1	AJ001367	Daucus carota small GTP-binding protein. Dc-Rab8.
CAA90080.1	Z49900	Pisum sativum small GTP-binding protein.
AAD46405.1	AF096249	Lycopersicon esculentum ethylene-responsive small GTP-binding protein. ER43.
CAA98174.1	Z73946	Lotus japonicus GTP-binding protein. RAB8C. rab8C.
CAA90082.1	Z49902	Pisum sativum small GTP-binding protein.
CAA49600.1	X69980	Lycopersicon esculentum GTP-binding protein. ypt2.
CAA98175.1	Z73947	Lotus japonicus GTP-binding protein. RAB8D. rab8D.
CAA90081.1	Z49901	Pisum sativum small GTP-binding protein.
AAB17726.1	U38471	Brassica rapa small GTP-binding protein rab. BRAB-1. small GTP-binding protein rab family.
AAA34251.1	L08128	Volvox carteri GTP-binding protein. yptV2.
CAA98173.1	Z73945	Lotus japonicus GTP-binding protein. RAB8B. rab8B.
CAA89049.1	Z49190	Beta vulgaris GTP-binding. small G protein.
CAA98179.1	Z73951	Lotus japonicus GTP-binding protein. RAB11C. rab11C.
AAA34253.1	L08130	Volvox carteri GTP-binding protein. yptV4.

CAA98165.1	Z73937	Lotus japonicus GTP-binding protein. RAB2A. rab2A.
AAA63902.1	U22433	Zea mays GTP binding protein. rab2.
AAA90955.1	U32185	Glycine max vesicular transport. guanine nucleotide regulatory protein. rab2. GTP-binding protein; soyrab. SEQ ID NO: 628
AAA87456.1	U22147	Hevea brasiliensis beta-1,3-glucanase. HGN1. hydrolytic enzyme.
CAB38443.1	AJ133470	Hevea brasiliensis beta-1,3-glucanase. hgn1.
AAG24921.1	AF311749	Hevea brasiliensis beta-1,3-glucanase.
AAF44667.1	AF239617	Vitis vinifera hydrolysis of 1,3-beta-D-glucosidic linkages in 1,3-beta-D-glucans. beta-1,3-glucanase. fungal pathogen defense-related protein.
AAA33648.1	L02212	Pisum sativum beta-1,3-glucan hydrolysis. beta-1,3-glucanase. putative.
AAB41551.1	U27179	Medicago sativa subsp. sativa acidic glucanase.
AAB24398.1	S51479	Pisum sativum beta-1,3-glucanase. beta-1,3-glucanase. This sequence comes from Fig. 1B.
CAA37289.1	X53129	Phaseolus vulgaris 1,3,-beta-D-glucanase.
AAA34078.1	M63634	Nicotiana plumbaginifolia regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.
AAA51643.1	M23120	Nicotiana plumbaginifolia beta-glucanase precursor.
CAA30261.1	X07280	Nicotiana plumbaginifolia beta-glucanase.
AAA03618.1	M80608	Lycopersicon esculentum beta-1,3-glucanase.
AAC19114.1	AF067863	Solanum tuberosum 1,3-beta-glucan glucanohydrolase. glucanase.
AAA18928.1	U01901	Solanum tuberosum catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). glub2. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAA63539.1	M60402	Nicotiana tabacum glucan beta-1,3-glucanase. glucanase GLA.
AAA63540.1	M60403	Nicotiana tabacum glucan-1,3-beta-glucosidase. glucanase GLB.

AAA88794.1	U01900	Solanum tuberosum
catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB1. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.		
AAA63541.1	M59442	Nicotiana tabacum
basic beta-1,3-glucanase, glucanase.		
AAB82772.2	AF001523	Musa acuminata
beta-1,3-glucanase. similar to beta-1,3-glucanase.		
AAF08679.1	AF004838	Musa acuminata
beta-1,3-glucanase.		
AAA19111.1	U01902	Solanum tuberosum
catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB3. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.		
AAC04710.1	AF034106	Glycine max
beta-1,3-glucanase 1. SGlu1.		
AAC04714.1	AF034113	Glycine max
beta-1,3-glucanase 8. SGlu8.		
CAB91554.1	AJ277900	Vitis vinifera
beta 1-3 glucanase. g1.		
AAA34082.1	M20620	Nicotiana tabacum
prepro-beta-1,3-glucanase precursor.		
CAA03908.1	AJ000081	Citrus sinensis
glucan hydrolase. beta-1,3-glucanase. gns1.		
AAB03501.1	U41323	Glycine max
beta-1,3-glucanase. SGN1.		
AAA92013.1	U49454	Prunus persica
beta-1,3-glucanase. Gns1.		
AAA33946.1	M37753	Glycine max
beta-1,3-endoglucanase (EC 3.2.1.39).		
AAA63542.1	M59443	Nicotiana tabacum
acidic beta-1,3-glucanase. glucanase.		
AAF34761.1	AF227953	Capsicum annuum
basic beta-1,3-glucanase. BGLU.		
AAD33881.1	AF141654	Nicotiana tabacum
beta-1,3-glucanase. GGL4.		
AAG34080.1	AF294849	Capsicum annuum
beta-1,3-glucanase-like protein.		
AAF33405.1	AF230109	Populus x canescens
beta-1,3 glucanase. BGLUC.		

AAD33880.1 AF141653 Nicotiana tabacum
beta-1,3-glucanase. GGL1.

CAA57255.1 X81560 Nicotiana tabacum
(1-)-beta-glucanase. Sp41a.

AAA34053.1 M60464 Nicotiana tabacum
beta-1,3-glucanase.

SEQ ID NO: 630

AAD37698.1 AF145729 Oryza sativa
homeodomain leucine zipper protein. Oshox5. transcription factor.

BAA05624.1 D26575 Daucus carota
transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.

AAF01765.1 AF184278 Glycine max
homeodomain-leucine zipper protein 57. Hdl57. transcription factor.

CAA64417.1 X94947 Lycopersicon esculentum
homeobox. VAHOX1.

BAA93465.1 AB028077 Physcomitrella patens
homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.

BAB18171.1 AB042769 Zinnia elegans
homeobox-leucine zipper protein. ZeHB3. full length.

BAA93460.1 AB028072 Physcomitrella patens
homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.

BAA93466.1 AB028078 Physcomitrella patens
homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.

BAA93461.1 AB028073 Physcomitrella patens
homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.

BAA05625.1 D26576 Daucus carota
transcriptiional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.

BAA05622.1 D26573 Daucus carota
transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.

BAA93467.1 AB028079 Physcomitrella patens
homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.

BAA93464.1 AB028076 Physcomitrella patens
homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.

AAD37697.1 AF145728 Oryza sativa
homeodomain leucine zipper protein. Oshox4. transcription factor.

AAF01764.2 AF184277 Glycine max
homeodomain-leucine zipper protein 56. Hdl56. transcription factor.

BAA21017.1 D26578 Daucus carota
transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.

BAB18168.1	AB042766	Zinnia elegans homeobox-leucine zipper protein. ZeHB7. 3'RACE product.
BAA93468.1	AB028080	Physcomitrella patens homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.
BAA05623.1	D26574	Daucus carota transcriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.
AAD37699.1	AF145730	Oryza sativa homeodomain leucine zipper protein. Oshox6. transcription factor.
AAD38144.1	AF139497	Prunus armeniaca DNA-binding protein. homeobox leucine zipper protein. HBLZP.
AAA63768.2	AF339748	Helianthus annuus homeobox-leucine zipper protein HAHB-4. Hahb-4.
BAA93463.1	AB028075	Physcomitrella patens homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
CAA64491.1	X95193	Pimpinella brachycarpa transcription activator. homeobox-leucine zipper protein.
CAA64221.1	X94449	Pimpinella brachycarpa transcription activator. homeobox-leucine zipper protein. PHZ4.
CAA64152.1	X94375	Pimpinella brachycarpa transcription activator. homeobox-leucine zipper protein.
AAD37700.1	AF145731	Oryza sativa homeodomain leucine zipper protein. Oshox7. transcription factor.
AAD37695.1	AF145726	Oryza sativa homeodomain leucine zipper protein. Oshox2. transcription factor.
CAA06728.1	AJ005833	Craterostigma plantagineum transcription factor. homeodomain leucine zipper protein. hb-2.
CAA62608.1	X91212	Lycopersicon esculentum HD-ZIP protein. THOM1.
CAA63222.1	X92489	Glycine max transcription activator. homeobox-leucine zipper protein.
CAA65456.2	X96681	Oryza sativa transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.
AAF19980.1	AF211193	Oryza sativa homeodomain-leucine zipper transcription factor. Hox1. hox1.
SEQ ID NO: 631		
CAC19183.1	AJ291816	Cicer arietinum expansin.
AAD13633.1	AF059489	Lycopersicon esculentum expansin precursor. Exp5.
AAG13983.1	AF297522	Prunus avium expansin 2. Exp2. PruavExp2.

AAF35902.1 AF230333 *Zinnia elegans*
expansin 3.

AAF32409.1 AF230276 *Triphysaria versicolor*
alpha-expansin 3.

AAC96080.1 AF049353 *Nicotiana tabacum*
involved in acid-growth response. alpha-expansin precursor. Nt-EXP4. cell wall protein.

AAG13982.1 AF297521 *Prunus avium*
expansin 1. Exp1. PruavExp1.

AAC33529.1 U93167 *Prunus armeniaca*
expansin. PA-Exp1.

AAF32411.1 AF230278 *Triphysaria versicolor*
alpha-expansin 1.

AAF35901.1 AF230332 *Zinnia elegans*
expansin 2.

AAF21101.1 AF159563 *Fragaria x ananassa*
expansin. Exp2. ripening regulated.

BAB19676.1 AB029083 *Prunus persica*
expansin. PchExp1.

AAD47901.1 AF085330 *Pinus taeda*
expansin.

AAC33530.1 AF038815 *Prunus armeniaca*
expansin. Exp2.

CAC19184.1 AJ291817 *Cicer arietinum*
expansin.

AAB40635.1 U64891 *Pinus taeda*
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAG32921.1 AF184233 *Lycopersicon esculentum*
expansin. Exp10.

AAD49956.1 AF167360 *Rumex palustris*
expansin. EXP1.

AAB40637.1 U64893 *Pinus taeda*
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAB40634.1 U64890 *Pinus taeda*
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAB37746.1	U30382	Cucumis sativus expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.
AAB40636.1	U64892	Pinus taeda expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAC39512.1	AF043284	Gossypium hirsutum expansin. GhEX1. contains N-terminal signal peptide.
CAB43197.1	AJ239068	Lycopersicon esculentum cell wall loosening enzyme. expansin2. exp2.
AAC64201.1	AF096776	Lycopersicon esculentum expansin. LeEXP2.
AAC96081.1	AF049354	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.
CAB46492.1	AJ243340	Lycopersicon esculentum expansin9. exp9.
AAF17570.1	AF202119	Marsilea quadrifolia alpha-expansin. EXP1. Mq-EXP1.
AAB81662.1	U85246	Oryza sativa expansin. Os-EXP4.
AAF62180.1	AF247162	Oryza sativa alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.
AAB38074.1	U30477	Oryza sativa induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.
AAD13632.1	AF059488	Lycopersicon esculentum expansin precursor. Exp4.
AAF32410.1	AF230277	Triphysaria versicolor alpha-expansin 2.
AAG01875.1	AF291659	Striga asiatica alpha-expansin 3. Exp3.
CAA04385.1	AJ000885	Brassica napus Cell wall extension in plants. Expansin.
CAA06271.2	AJ004997	Lycopersicon esculentum expansin18. exp18.
BAB32732.1	AB049406	Eustoma grandiflorum expansin. Eg Expansin.
AAC63088.1	U82123	Lycopersicon esculentum expansin. LeEXP1. fruit ripening regulated expansin.

AAF62182.1 AF247164	Oryza sativa alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.
AAB37749.1 U30460	Cucumis sativus expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAG32920.1 AF184232	Lycopersicon esculentum expansin. Exp8.
CAC06433.1 AJ276007	Festuca pratensis expansin. exp2.
AAF62181.1 AF247163	Oryza sativa alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.
AAC96079.1 AF049352	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
AAC96077.1 AF049350	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
BAA88200.1 AP000837	Oryza sativa EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAF17571.1 AF202120	Regnellidium diphyllum alpha-expansin. EXP1. Rd-EXP1.
AAC96078.1 AF049351	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
AAG01874.1 AF291658	Striga asiatica alpha-expansin 2. Exp2.

SEQ ID NO: 634

AAF63205.1 AF245119	Mesembryanthemum crystallinum AP2-related transcription factor. CDBP. stress induced transcription factor.
BAA97122.1 AB016264	Nicotiana sylvestris ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
BAA07321.1 D38123	Nicotiana tabacum ERF1. ethylene-responsive transcription factor.
AAG43545.1 AF211527	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
BAA87068.1 AB035270	Matricaria chamomilla ethylene-responsive element binding protein1 homolog. McEREBP1.
BAA97124.1 AB016266	Nicotiana sylvestris ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
AAC62619.1 AF057373	Nicotiana tabacum transcription factor. ethylene response element binding protein 1. EREBP1.
CAB93940.1 AJ238740	Catharanthus roseus putative transcription factor. AP2-domain DNA-binding protein. orca2.

AAK31279.1	AC079890	Oryza sativa putative ethylene-responsive element binding protein. OSJNBb0089A17.16.
AAG60182.1	AC084763	Oryza sativa putative ethylene-responsive element binding protein. OSJNBA0027P10.12.
CAB96900.1	AJ251250	Catharanthus roseus transcription factor. AP2-domain DNA-binding protein. orca3.
CAB96899.1	AJ251249	Catharanthus roseus transcription factor. AP2-domain DNA-binding protein. orca3.
CAC12822.1	AJ299252	Nicotiana tabacum AP2 domain-containing transcription factor. ap2.
AAF23899.1	AF193803	Oryza sativa transcription factor EREBP1. EREBP/AP2-like transcription factor.
AAF05606.1	AF190770	Oryza sativa EREBP-like protein. tsh1. TSH1; induced by ethylene.
BAA97123.1	AB016265	Nicotiana sylvestris ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
BAA76734.1	AB024575	Nicotiana tabacum ethylene responsive element binding factor.
BAB03248.1	AB037183	Oryza sativa ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
CAB93939.1	AJ238739	Catharanthus roseus putative transcription factor. AP2-domain DNA-binding protein. orca1.
AAD00708.1	U91857	Stylosanthes hamata ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
AAG43548.1	AF211530	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
AAG43549.1	AF211531	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
AAK31271.1	AC079890	Oryza sativa putative transcriptional factor. OSJNBb0089A17.22.
AAK01088.1	AF298230	Hordeum vulgare CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
AAC49567.1	U41466	Zea mays Glossy15. Glossy15. AP2 DNA-binding domain protein; similar to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.
SEQ ID NO: 635		
CAC19789.1	AJ251686	Catharanthus roseus putative transcription factor. MYB-like DNA-binding protein. bpf-1.

CAA55693.1 X79086 Zea mays
initiator-binding protein. IBP2.

CAA55691.1 X79085 Zea mays
initiator binding protein. IBP1.

AAF97508.1 AF242298 Oryza sativa
telomere binding protein-1. TBP1.

SEQ ID NO: 636

CAB43505.1 AJ239051 Cicer arietinum
cytochrome P450. cyp81E2.

BAA22422.1 AB001379 Glycyrrhiza echinata
cytochrome P450. CYP81E1.

BAA74465.1 AB022732 Glycyrrhiza echinata
cytochrome P450. CYP Ge-31.

CAA10067.1 AJ012581 Cicer arietinum
cytochrome P450. cyp81E3.

CAB41490.1 AJ238439 Cicer arietinum
cytochrome P450 monooxygenase. cyp81E3v2.

BAA93634.1 AB025016 Lotus japonicus
cytochrome P450.

CAA04117.1 AJ000478 Helianthus tuberosus
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11. chimeric sequence (from 5'-race).

CAA04116.1 AJ000477 Helianthus tuberosus
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

AAK38080.1 AF321856 Lolium rigidum
putative cytochrome P450.

AAK38079.1 AF321855 Lolium rigidum
putative cytochrome P450.

AAK38081.1 AF321857 Lolium rigidum
putative cytochrome P450.

AAC34853.1 AF082028 Hemerocallis hybrid cultivar
putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3.
mRNA accumulates in senescing petals.

CAA65580.1 X96784 Nicotiana tabacum
cytochrome P450. hsr515.

CAB56742.1 AJ249800 Cicer arietinum
cytochrome P450 monooxygenase. cyp81E5.

AAA32913.1 M32885 Persea americana
cytochrome P-450LXXIA1 (cyp71A1).

BAA12159.1 D83968 Glycine max
Cytochrome P-450 (CYP93A1).

AAD56282.1 AF155332 Petunia x hybrida
flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

CAA71515.1	Y10491	Glycine max putative cytochrome P450.
AAB94590.1	AF022461	Glycine max CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
CAA71516.1	Y10492	Glycine max putative cytochrome P450.
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
BAA13076.1	D86351	Glycine max cytochrome P-450 (CYP93A2).
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
AAG09208.1	AF175278	Pisum sativum wound-inducible P450 hydroxylase. CYP82A1.
AAC49188.2	U29333	Pisum sativum cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
AAD38930.1	AF135485	Glycine max cytochrome P450 monooxygenaseCYP93D1. CYP93E1.
CAA71876.1	Y10982	Glycine max putative cytochrome P450.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
CAA70576.1	Y09424	Nepeta racemosa cytochrome P450. CYP71A6.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
CAA71877.1	Y10983	Glycine max putative cytochrome P450.
AAB94587.1	AF022458	Glycine max CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAC39454.1	AF014802	Eschscholzia californica (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to wound-inducible CYP82A1 of Pisum sativum GenBank Accession Number U29333.
BAA92894.1	AB006790	Petunia x hybrida cytochrome P450. IMT-2.
BAA84072.1	AB028152	Torenia hybrida flavone synthase II. cytochrome P450. TFNS5.
BAA35080.1	AB015762	Nicotiana tabacum putative cytochrome P450. CYP82E1.
CAB56743.1	AJ249801	Cicer arietinum cytochrome P450 monooxygenase. cyp81E4.

AAB17562.1 U72654 *Eustoma grandiflorum*
flavonoid 3'S'-hydroxylase. F3'S'H. cytochrome P450; CYP75.

AAG34695.1 AF313492 *Matthiola incana*
putative cytochrome P450.

BAA74466.1 AB022733 *Glycyrrhiza echinata*
cytochrome P450. CYP Ge-51.

BAA22423.1 AB001380 *Glycyrrhiza echinata*
cytochrome P450. CYP93B1.

SEQ ID NO: 639

AAC06319.1 AF053084 *Malus x domestica*
putative cinnamyl alcohol dehydrogenase. CAD.

CAA61275.1 X88797 *Eucalyptus gunnii*
cinnamyl alcohol dehydrogenase. CAD1.

SEQ ID NO: 640

BAA92916.1 AP001539 *Oryza sativa*

EST C26826(C50159) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC F13A10; putative ARF1 family auxin responsive transcription factor. (AC006418).

AAK21342.1 AC024594 *Oryza sativa*
putative transcription factor. OSJNBa0093B11.2.

AAG43286.1 AF140228 *Oryza sativa*
auxin response factor 1.

SEQ ID NO: 641

CAC24691.1 AJ132363 *Brassica juncea*
efflux carrier of polar auxin transport. pina.

AAG17172.1 AF190881 *Populus tremula x Populus tremuloides*
PIN1-like auxin transport protein. ppl1.

AAC39514.1 AF056027 *Oryza sativa*
auxin transport protein REH1. REH1. potential membrane protein.

SEQ ID NO: 642

AAG22044.1 AF305783 *Pisum sativum*
apyrase 2. apy2. phosphatase.

AAF00610.1 AF156781 *Dolichos biflorus*
apyrase. apyrase-2.

AAG32959.1 AF207687 *Glycine soja*
apyrase GS50.

AAG32960.1 AF207688 *Glycine soja*
apyrase GS52.

AAF00609.1 AF156780 *Lotus japonicus*
apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.

AAD31285.1 AF139807 *Dolichos biflorus*
apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.

AAF00611.1 AF156782	Medicago sativa apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
AAK15160.1 AF288132	Medicago truncatula putative apyrase. apy1. nucleotide phosphohydrolase; Mtapy1.
BAB18896.1 AB038669	Pisum sativum apyrase.
BAB18895.1 AB038668	Pisum sativum apyrase.
BAB18894.1 AB038555	Pisum sativum apyrase H-type.
BAB18893.1 AB038554	Pisum sativum apyrase S-type.
BAB18900.1 AB027614	Pisum sativum apyrase.
BAB40230.1 AB027613	Pisum sativum S-type apyras. ATP diphosphohydrolase (apyrase) S-type.
BAB18890.1 AB023621	Pisum sativum apyrase S-type. ATP diphosphohydrolase (apyrase) S-type.
BAA75506.1 AB022319	Pisum sativum apyrase. cytoskeleton associated.
BAA89275.1 AB027616	Pisum sativum apyrase.
BAB40231.1 AB027615	Pisum sativum S-type apyrase. ATP diphosphohydrolase (apyrase) S-type.
AAB02720.1 U58597	Solanum tuberosum catalyzes the hydrolysis of phosphoanhydride bonds of nucleoside tri- and di- phosphates in the presence of divalent cations. ATP-diphosphohydrolase. RROP1. apyrase, Ecto-ATPase, E-type ATPase; NTP-diphosphohydrolase.
AAK15161.1 AF288133	Medicago truncatula putative apyrase. apy4. nucleotide phosphohydrolase; Mtapy4.
BAB18891.1 AB030444	Pisum sativum apyrase. ATP diphosphohydrolase, (EC 3.6.1.5) this sequence is reported in Acc#:AB022319.
BAB18892.1 AB030445	Pisum sativum apyrase. ATP diphosphohydrolase, EC 3.6.1.5 this sequence is reported in Acc#:AB022319, Acc#:AB027613.
SEQ ID NO: 645	
AAG22044.1 AF305783	Pisum sativum apyrase 2. apy2. phosphatase.
AAF00610.1 AF156781	Dolichos biflorus apyrase. apyrase-2.
AAG32959.1 AF207687	Glycine soja apyrase GS50.

AAG32960.1	AF207688	Glycine soja apyrase GS52.
AAD31285.1	AF139807	Dolichos biflorus apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
AAK15160.1	AF288132	Medicago truncatula putative apyrase. apy1. nucleotide phosphohydrolase; Mtapy1.
AAF00609.1	AF156780	Lotus japonicus apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
BAB18896.1	AB038669	Pisum sativum apyrase.
BAB18895.1	AB038668	Pisum sativum apyrase.
BAB18894.1	AB038555	Pisum sativum apyrase H-type.
BAB18893.1	AB038554	Pisum sativum apyrase S-type.
BAB18900.1	AB027614	Pisum sativum apyrase.
BAB40230.1	AB027613	Pisum sativum S-type apyras. ATP diphosphohydrolase (apyrase) S-type.
BAB18890.1	AB023621	Pisum sativum apyrase S-type. ATP diphosphohydrolase (apyrase) S-type.
BAA75506.1	AB022319	Pisum sativum apyrase. cytoskeleton associated.
AAF00611.1	AF156782	Medicago sativa apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
BAA89275.1	AB027616	Pisum sativum apyrase.
BAB40231.1	AB027615	Pisum sativum S-type apyrase. ATP diphosphohydrolase (apyrase) S-type.
AAB02720.1	U58597	Solanum tuberosum catalyzes the hydrolysis of phosphoanhydride bonds of nucleoside tri- and di- phosphates in the presence of divalent cations. ATP-diphosphohydrolase. RROP1. apyrase, Ecto-ATPase, E-type ATPase; NTP-diphosphohydrolase.
AAK15161.1	AF288133	Medicago truncatula putative apyrase. apy4. nucleotide phosphohydrolase; Mtapy4.
BAB18891.1	AB030444	Pisum sativum apyrase. ATP diphosphohydrolase, (EC 3.6.1.5) this sequence is reported in Acc#:AB022319.
BAB18892.1	AB030445	Pisum sativum apyrase. ATP diphosphohydrolase, EC 3.6.1.5 this sequence is reported in Acc#:AB022319, Acc#:AB027613.

SEQ ID NO: 646

AAB80947.1	AF022915	Triticum aestivum ornithine/acetylornithine aminotransferase.
CAA69936.1	Y08680	Alnus glutinosa acetylornithine aminotransferase. ag118.
AAK11219.1	AF324485	Oryza sativa aminotransferase-like protein.
AAG09278.1	AF177590	Vitis vinifera ornithine aminotransferase.
AAC78480.1	AF085149	Capsicum chinense putative aminotransferase. pyridoxal phosphate dependent.
AAA02916.1	L08400	Vigna aconitifolia production of pyrroline-5-carboxylate by deamination of ornithine. ornithine aminotransferase.
AAB59330.1	M31545	Hordeum vulgare glutamate 1-semialdehyde aminotransferase. GSA. precursor.
AAA18861.1	U03632	Chlamydomonas reinhardtii glutamate-1-semialdehyde aminotransferase. gsa.
AAA33968.1	L12453	Glycine max catalyzes 5-aminolevulinic acid formation from GSA. glutamate 1-semialdehyde aminotransferase. Gsa. putative.
AAC48996.1	U20260	Glycine max converts GSA to 5-aminolevulinic acid. glutamate 1-semialdehyde aminotransferase. Gsa1.
SEQ ID NO: 650		
AAF66982.1	AF247646	Zea mays transposase. similar to Mutator family transposases.
SEQ ID NO: 652		
AAB41812.1	L36158	Medicago sativa peroxidase. pxdD. amino acid feature: conserved domains, aa 120 .. 126, 188 .. 195; amino acid feature: heme-binding domain, aa 63 .. 68.
CAA71495.1	Y10469	Spinacia oleracea peroxidase. prxr8.
CAA09881.1	AJ011939	Trifolium repens peroxidase. prx2.
CAA62228.1	X90695	Medicago sativa peroxidase2. prx2.
AAA98491.1	L36981	Petroselinum crispum anionic peroxidase.
BAB39281.1	AP002971	Oryza sativa putative peroxidase. P0537A05.10. contains ESTs D24657(R2329),AU082066(R2329).
AAB02926.1	U59284	Linum usitatissimum peroxidase. FLXPER3.
BAA77387.1	AB024437	Scutellaria baicalensis peroxidase 1.

CAA66037.1	X97351	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i> signal for ER. peroxidase.
CAA71488.1	Y10462	<i>Spinacia oleracea</i> peroxidase. <i>prxr1</i> .
BAA01950.1	D11337	<i>Vigna angularis</i> peroxidase.
BAA14143.1	D90115	<i>Armoracia rusticana</i> peroxidase isozyme.
CAA71490.1	Y10464	<i>Spinacia oleracea</i> peroxidase. <i>prxr3</i> .
CAB94692.1	AJ242742	<i>Ipomoea batatas</i> Removal of H ₂ O ₂ , oxidation of toxic reductants, defence response toward wounding. peroxidase. <i>pod</i> .
BAA92497.1	AP001383	<i>Oryza sativa</i> ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to peroxidase ATP18a. (X98804).
AAC36707.1	AF078691	<i>Manihot esculenta</i> peroxidase.
BAA92422.1	AP001366	<i>Oryza sativa</i> ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to <i>A.thaliana</i> mRNA for peroxidase ATP18a. (X98804).
CAA62226.1	X90693	<i>Medicago sativa</i> peroxidase1B. <i>prx1B</i> .
AAF63024.1	AF244921	<i>Spinacia oleracea</i> hydrogen peroxide catabolism. peroxidase <i>prx12</i> precursor. type III peroxidase.
AAA32676.1	M37637	<i>Arachis hypogaea</i> cationic peroxidase. PNC2.
BAA11853.1	D83225	<i>Populus nigra</i> peroxidase.
CAC21393.1	AJ401276	<i>Zea mays</i> peroxidase. <i>pox3</i> .
AAA65636.1	L13653	<i>Lycopersicon esculentum</i> peroxidase. TPX2.
CAB67121.1	Y19023	<i>Lycopersicon esculentum</i> peroxidase. <i>cevi-1</i> .
CAA62227.1	X90694	<i>Medicago sativa</i> peroxidase1C. <i>prx1C</i> .
CAA50597.1	X71593	<i>Lycopersicon esculentum</i> peroxidase. CEVI-1.
AAD37376.1	AF145350	<i>Glycine max</i> peroxidase. <i>Prx4</i> .
AAB67737.1	L77080	<i>Stylosanthes humilis</i> cationic peroxidase.

CAA71489.1	Y10463	Spinacia oleracea peroxidase. prxr2.
CAA71496.1	Y10470	Spinacia oleracea peroxidase. prxr9.
CAA71494.1	Y10468	Spinacia oleracea peroxidase. prxr7.
BAA06334.1	D30652	Populus kitakamiensis peroxidase.
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA94962.1	AB042103	Asparagus officinalis peroxidase. AspPOX1.
CAA80502.1	Z22920	Spirodela polyrrhiza peroxidase.
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA11852.1	D83224	Populus nigra peroxidase.
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA07241.1	D38051	Populus kitakamiensis peroxidase. prxA4a.
AAD11481.1	U51191	Glycine max peroxidase precursor. sEPa1.
AAC98519.1	AF007211	Glycine max peroxidase precursor. GMIPER1. pathogen-induced.
AAA32973.1	M73234	Hordeum vulgare peroxidase BP 1. Prx5.
AAB47602.1	L07554	Linum usitatissimum peroxidase. FLXPER1.
AAB41810.1	L36156	Medicago sativa peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
AAF63027.1	AF244924	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
AAA34108.1	J02979	Nicotiana tabacum lignin-forming peroxidase precursor (EC 1.11.1.7).
AAD43561.1	AF155124	Gossypium hirsutum bacterial-induced peroxidase precursor. Perx_Goshiko.
SEQ ID NO: 653		

AAB97617.1	U83687	<i>Apium graveolens</i>
NADPH-dependent mannose 6-phosphate reductase. m6pr. aldo-keto reductase; similar to aldose 6-phosphate reductase also known as NADP-sorbitol-6-phosphate dehydrogenase encoded by GenBank Accession Number D11080.		
BAA01853.1	D11080	<i>Malus x domestica</i>
NADP-dependent D-sorbitol-6-phosphate dehydrogenase. S6PDH.		
AAC97607.1	AF057134	<i>Malus x domestica</i>
synthesizes sorbitol, a major photosynthetic product in many members of the Rosaceae family. NADP-dependent sorbitol 6-phosphate dehydrogenase. S6PDH.		
SEQ ID NO: 654		
BAA82556.1	AB030083	<i>Populus nigra</i>
lectin-like protein kinase. PnLPK.		
AAB61708.1	U93048	<i>Daucus carota</i>
somatic embryogenesis receptor-like kinase. SERK.		
BAB19337.1	AP003044	<i>Oryza sativa</i>
putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).		
AAK21965.1	AY028699	<i>Brassica napus</i>
receptor protein kinase PERK1.		
BAB39873.1	AP002882	<i>Oryza sativa</i>
putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).		
AAB93834.1	U82481	<i>Zea mays</i>
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.		
BAB18292.1	AP002860	<i>Oryza sativa</i>
putative receptor-like protein kinase. P0409B08.19.		
AAK00425.1	AC069324	<i>Oryza sativa</i>
Putative protein kinase. OSJNBa0071K19.11.		
AAD21872.1	AF078082	<i>Phaseolus vulgaris</i>
receptor-like protein kinase homolog RK20-1.		
AAC23542.1	U20948	<i>Ipomoea trifida</i>
receptor protein kinase. IRK1.		
CAA73134.1	Y12531	<i>Brassica oleracea</i>
serine/threonine kinase. BRLK.		
CAB51480.1	Y14600	<i>Sorghum bicolor</i>
putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.		
AAG59657.1	AC084319	<i>Oryza sativa</i>
putative protein kinase. OSJNBa0004B24.20.		
BAB16871.1	AP002537	<i>Oryza sativa</i>
putative protein kinase APK1A <i>Arabidopsis thaliana</i> . P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).		

CAB51834.1	00069	Oryza sativa
l1332.5. contains eukaryotic protein kinase domain PF.		
BAA94509.1	AB041503	Populus nigra
protein kinase 1. PnPK1.		
AAG16628.1	AY007545	Brassica napus
protein serine/threonine kinase BNK1.		
BAA87853.1	AP000816	Oryza sativa
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).		
BAB03429.1	AP002817	Oryza sativa
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).		
BAB07999.1	AP002525	Oryza sativa
putative protein kinase. P0462H08.22. contains EST C22619(S11214).		
BAB21240.1	AP002953	Oryza sativa
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).		
BAA92954.1	AP001551	Oryza sativa
Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).		
BAA94510.1	AB041504	Populus nigra
protein kinase 2. PnPK2.		
AAG03090.1	AC073405	Oryza sativa
Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).		
AAF91322.1	AF244888	Glycine max
receptor-like protein kinase 1. RLK1. GmRLK1.		
BAA94517.1	AP001800	Oryza sativa
Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).		
BAB07905.1	AP002835	Oryza sativa
putative S-receptor kinase. P0417G05.13.		
CAB51836.1	AJ243961	Oryza sativa
Putitive Ser/Thr protein kinase. l1332.7.		
BAA78764.1	AB023482	Oryza sativa
ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).		
AAA33915.1	L27821	Oryza sativa
receptor type serine/threonine kinase. protein kinase.		
AAF91323.1	AF244889	Glycine max
receptor-like protein kinase 2. RLK2. GmRLK2.		
CAA67145.1	X98520	Brassica oleracea
receptor-like kinase. SFR2.		
CAA73133.1	Y12530	Brassica oleracea
serine /threonine kinase. ARLK.		
AAF91324.1	AF244890	Glycine max
receptor-like protein kinase 3. RLK3. GmRLK3.		

CAA74661.1 Y14285 Brassica oleracea
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

BAA92953.1 AP001551 Oryza sativa
Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).

BAB40094.1 AP003210 Oryza sativa
putative receptor protein kinase. OSJNBa0010K01.7.

AAF43496.1 AF131222 Lophopyrum elongatum
protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.

AAK11674.1 AF339747 Lophopyrum elongatum
protein kinase. ESI47.

BAB07906.1 AP002835 Oryza sativa
putative S-receptor kinase. P0417G05.14.

BAA94516.1 AP001800 Oryza sativa
Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).

CAB41878.1 Y18259 Brassica oleracea
SRK5 protein. SRK5. receptor-like kinase.

BAA23676.1 AB000970 Brassica rapa
receptor kinase 1. BcRK1.

CAB41879.1 Y18260 Brassica oleracea
SRK15 protein. SRK15. receptor-like kinase.

SEQ ID NO: 655

AAD21872.1 AF078082 Phaseolus vulgaris
receptor-like protein kinase homolog RK20-1.

CAA73134.1 Y12531 Brassica oleracea
serine/threonine kinase. BRLK.

CAA67145.1 X98520 Brassica oleracea
receptor-like kinase. SFR2.

CAA73133.1 Y12530 Brassica oleracea
serine /threonine kinase. ARLK.

AAB93834.1 U82481 Zea mays
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

BAA23676.1 AB000970 Brassica rapa
receptor kinase 1. BcRK1.

AAC23542.1 U20948 Ipomoea trifida
receptor protein kinase. IRK1.

CAB41879.1 Y18260 Brassica oleracea
SRK15 protein. SRK15. receptor-like kinase.

CAA74662.1	Y14286	Brassica oleracea
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.		
CAB89179.1	AJ245479	Brassica napus subsp. napus
ser /thr kinase. S-locus receptor kinase. srk.		
AAA33008.1	M97667	Brassica napus
serine/threonine kinase receptor.		
AAA62232.1	U00443	Brassica napus
S-receptor kinase. protein contains an immunoglobulin-like domain.		
CAA74661.1	Y14285	Brassica oleracea
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.		
AAA33000.1	M76647	Brassica oleracea
receptor protein kinase. SKR6.		
CAA79355.1	Z18921	Brassica oleracea
S-receptor kinase-like protein.		
CAB41878.1	Y18259	Brassica oleracea
SRK5 protein. SRK5. receptor-like kinase.		
BAA07576.1	D38563	Brassica rapa
receptor protein kinase SRK8.		
BAA06285.1	D30049	Brassica rapa
S-receptor kinase SRK9.		
BAA21132.1	D88193	Brassica rapa
S-receptor kinase. SRK9 (B.c.).		
BAA07577.2	D38564	Brassica rapa
receptor protein kinase SRK12.		
BAA92836.1	AB032473	Brassica oleracea
S18 S-locus receptor kinase. SRK18.		
BAB21001.1	AB054061	Brassica rapa
S locus receptor kinase. SRK22.		
BAA92837.1	AB032474	Brassica oleracea
S60 S-locus receptor kinase. SRK60.		
BAB18292.1	AP002860	Oryza sativa
putative receptor-like protein kinase. P0409B08.19.		
AAD52097.1	AF088885	Nicotiana tabacum
receptor-like kinase CHRK1. Chrk1.		
BAB39873.1	AP002882	Oryza sativa
putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).		
AAK21965.1	AY028699	Brassica napus
receptor protein kinase PERK1.		
AAA33915.1	L27821	Oryza sativa
receptor type serine/threonine kinase. protein kinase.		

AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
BAA94529.2	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAF34428.1	AF172282	Oryza sativa receptor-like protein kinase. DUPR11.18.
AAG03090.1	AC073405	Oryza sativa Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAA94516.1	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.13.
BAB07906.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.14.
SEQ ID NO: 657		
AAF43869.1	AF166114	Chloroplast Mesostigma viride probable transport protein. cysA.
BAB17113.1	AP002866	Oryza sativa putative white protein; ATP-binding cassette transporter. P0410E01.34.
BAA57907.1	AB001684	Chlorella vulgaris sulfate transport system permease protein. cysA.
AAD54843.1	AF137379	Chloroplast Nephroselmis olivacea probable transport protein. cysA.
BAA90508.1	AP001111	Oryza sativa similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAA90507.1	AP001111	Oryza sativa similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAA83352.1	AP000391	Oryza sativa ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.; Similar to ABC transporter-7 (U43892).
AAG49003.1	AY013246	Hordeum vulgare putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and comparative sequence.
AAD10836.1	U52079	Solanum tuberosum P-glycoprotein. pmdr1. binds ATP; ATPase; transporter; transmembrane protein.

BAA96612.1	AP002482	Oryza sativa Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ; putative ABC transporter (AC004411).
BAB40032.1	AP003046	Oryza sativa putative ABC transporter. P0445D12.3.
AAG45492.1	AY013245	Oryza sativa 36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and comparative sequence.
AAG49002.1	AY013246	Hordeum vulgare putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative sequencing.
BAB21275.1	AP002844	Oryza sativa putative ABC transporter protein. P0410E03.6.
BAB21273.1	AP002844	Oryza sativa putative ABC transporter protein. P0410E03.4.
CAA94437.1	Z70524	Spirodela polyrrhiza multidrug resistance protein. PDR5-like ABC transporter.
BAB21276.1	AP002844	Oryza sativa putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
BAB21279.1	AP002844	Oryza sativa putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463),AU101680(R3463).
SEQ ID NO: 658		
AAD10386.1	U72255	Oryza sativa beta-1,3-glucanase precursor. Gns9.
BAA89481.1	AB029462	Salix gilgiana beta-1,3-glucanase. SgGN1.
CAB85903.1	AJ251646	Pisum sativum hydrolysis of beta-1,3 conjugated glucans. beta-1,3 glucanase. gns2.
CAA49513.1	X69887	Brassica napus beta-1,3-glucanase homologue.
AAA90953.1	U30323	Triticum aestivum beta 1,3-glucanase. Glc1.
BAB19363.1	AP002542	Oryza sativa putative beta-1,3-glucanase. P0679C08.2.
CAA82271.1	Z28697	Nicotiana tabacum beta-1,3-glucanase.
CAA30261.1	X07280	Nicotiana plumbaginifolia beta-glucanase.
AAA51643.1	M23120	Nicotiana plumbaginifolia beta-glucanase precursor.
AAA34078.1	M63634	Nicotiana plumbaginifolia regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.

AAB82772.2	AF001523	Musa acuminata beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
AAF08679.1	AF004838	Musa acuminata beta-1,3-glucanase.
CAB71021.1	AJ271598	Hieracium piloselloides putative role in callose degradation. putative beta-1,3-glucanase. gluc.
AAD10383.1	U72252	Oryza sativa beta-1,3-glucanase precursor. Gns6.
AAD28732.1	AF112965	Triticum aestivum beta-1,3-glucanase precursor. Glb3.
BAB40807.1	AB052291	Pyrus pyrifolia catalyzing the hydrolysis of 1,3-beta-glucosyl linkages. endo-1,3-beta-glucanase-like protein. bgn-1. Amino acid alignment of the protein(BGN-1) encoded by pear pollen bgn-1 with barley endo-1,3-beta-glucanase(GII. accession number:pdb/1GHS-B/2.3/2/306/N/(40% identity) and their hydrophobic cluster analysis(HCA)(a overall HCA homology score of 87.1%) showed that it was most likely that the bgn-1 encoded a endo-1,3-beta-glucanase. A higher identity(59.3%) was found between BGN-1 and a putative pea endo-1,3-beta-glucanase (accession number:dad/AJ251646-1).
AAA63539.1	M60402	Nicotiana tabacum glucan beta-1,3-glucanase. glucanase GLA.
AAA63541.1	M59442	Nicotiana tabacum basic beta-1,3-glucanase. glucanase.
AAA63540.1	M60403	Nicotiana tabacum glucan-1,3-beta-glucosidase. glucanase GLB.
AAA32939.1	M62907	Hordeum vulgare hydrolysis of beta-(1-3)-glucan. (1-3)-beta-glucanase. cBGL32.
AAC14399.1	AF030771	Hordeum vulgare beta-1,3-glucanase 2. BGL32.
AAA87456.1	U22147	Hevea brasiliensis beta-1,3-glucanase. HGN1. hydrolytic enzyme.
BAA77784.1	AB027429	Oryza sativa beta-1,3-glucanase.
BAA77785.1	AB027430	Oryza sativa beta-1,3-glucanase.
CAB91554.1	AJ277900	Vitis vinifera beta 1-3 glucanase. g1.
AAD10381.1	U72250	Oryza sativa beta-1,3-glucanase precursor. Gns4.
AAA33946.1	M37753	Glycine max beta-1,3-endoglucanase (EC 3.2.1.39).
AAD33881.1	AF141654	Nicotiana tabacum beta-1,3-glucanase. GGL4.

AAB86541.1	AF030166	Oryza sativa glucanase. glu1.
AAD10384.1	U72253	Oryza sativa beta-1,3-glucanase precursor. Gns7.
CAB38443.1	AJ133470	Hevea brasiliensis beta-1,3-glucanase. hgn1.
AAB03501.1	U41323	Glycine max beta-1,3-glucanase. SGN1.
AAA18928.1	U01901	Solanum tuberosum catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). glub2. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAA88794.1	U01900	Solanum tuberosum catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB1. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAC19114.1	AF067863	Solanum tuberosum 1,3-beta-glucan glucanohydrolase. glucanase.
AAG24921.1	AF311749	Hevea brasiliensis beta-1,3-glucanase.
CAA03908.1	AJ000081	Citrus sinensis glucan hydrolase. beta-1,3-glucanase. gns1.
CAA37289.1	X53129	Phaseolus vulgaris 1,3,-beta-D-glucanase.
CAA57255.1	X81560	Nicotiana tabacum (1-)beta-glucanase. Sp41a.
SEQ ID NO: 659		
AAB65776.1	U97521	Vitis vinifera class IV endochitinase. VvChi4A.
AAB65777.1	U97522	Vitis vinifera class IV endochitinase. VvChi4B.
BAA03751.1	D16223	Oryza sativa endochitinase. Cht-3.
CAA30142.1	X07130	Solanum tuberosum endochitinase.
BAA03749.1	D16221	Oryza sativa endochitinase. Cht-1.
SEQ ID NO: 660		
AAF07221.1	AF072519	Nicotiana tabacum centrin. CEN1. caltractin; EF-hand domain calcium-binding protein.

AAF07222.1 AF072520 *Nicotiana tabacum*
centrin. CEN2. caltractin; EF-hand domain calcium-binding protein.

CAA49153.1 X69220 *Scherffelia dubia*
caltractin.

AAC04626.1 U92973 *Marsilea vestita*
calcium-binding protein. centrin. MvCen1. caltractin.

AAB67855.1 U53812 *Dunaliella salina*
caltractin-like protein.

CAA41039.1 X57973 *Chlamydomonas reinhardtii*
caltractin.

CAA31163.1 X12634 *Chlamydomonas reinhardtii*
caltractin (AA 1 - 169).

SEQ ID NO: 664

BAB16432.1 AB041520 *Nicotiana tabacum*
WRKY transcription factor Nt-SubD48. Nt-SubD48.

AAC49528.1 U56834 *Petroselinum crispum*
DNA-binding. WRKY3. WRKY-type DNA-binding protein.

AAD27591.1 AF121354 *Petroselinum crispum*
binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.

AAD32676.1 AF140553 *Avena sativa*
DNA-binding protein WRKY3. wrky3. putative transcription factor.

BAA77358.1 AB020023 *Nicotiana tabacum*
WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.

AAG46150.1 AC018727 *Oryza sativa*
putative DNA-binding protein. OSJNBa0056G17.18.

BAB40073.1 AP003074 *Oryza sativa*
putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).

BAB18313.1 AP002865 *Oryza sativa*
putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).

AAD38283.1 AC007789 *Oryza sativa*
putative WRKY DNA binding protein. OSJNBa0049B20.9.

BAA77383.1 AB020590 *Nicotiana tabacum*
transcription factor NtWRKY2.

BAA82107.1 AB022693 *Nicotiana tabacum*
transcription factor. NtWRKY1.

CAA88326.1 Z48429 *Avena fatua*
binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.

AAD32677.1 AF140554 *Avena sativa*
DNA-binding protein WRKY1. wrky1. putative transcription factor.

AAD55974.1 AF121353 *Petroselinum crispum*
zinc-finger type transcription factor WRKY1. WRKY1.

AAC49529.1	U58540	Petroselinum crispum WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
AAC49527.1	U48831	Petroselinum crispum WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.
AAC31956.1	AF080595	Pimpinella brachycarpa zinc finger protein. ZFP1. WRKY1.
BAA86031.1	AB026890	Nicotiana tabacum transcription factor NtWRKY4.
AAD16139.1	AF096299	Nicotiana tabacum DNA-binding protein 2. WRKY2. transcription factor.
AAF23898.1	AF193802	Oryza sativa zinc finger transcription factor WRKY1.
AAD16138.1	AF096298	Nicotiana tabacum DNA-binding protein 1. WRKY1. transcription factor.
AAC37515.1	L44134	Cucumis sativus SPF1-like DNA-binding protein.
AAG35658.1	AF204925	Petroselinum crispum transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.
CAA88331.1	Z48431	Avena fatua binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
BAB19075.1	AP002744	Oryza sativa putative DNA-binding protein homolog. P0006C01.17.
BAB19096.1	AP002839	Oryza sativa putative DNA-binding protein homolog. P0688A04.2.
AAK16170.1	AC079887	Oryza sativa putative DNA binding protein. OSJNBa0040E01.4.
AAK16171.1	AC079887	Oryza sativa putative DNA-binding protein. OSJNBa0040E01.10.
AAG35659.1	AF204926	Petroselinum crispum transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.
CAB97004.1	AJ278507	Solanum tuberosum putative transcription factor. WRKY DNA binding protein. WRKY1.
AAF61864.1	AF193771	Nicotiana tabacum DNA-binding protein 4. WRKY4. transcription factor.
BAA87069.1	AB035271	Matricaria chamomilla elicitor-induced DNA-binding protein homolog. McWRKY1.
AAF61863.1	AF193770	Nicotiana tabacum DNA-binding protein 3. WRKY3. transcription factor.
SEQ ID NO: 665		
AAD02558.1	AF049933	Petunia x hybrida PGPS/NH17. PGPS/NH17. protein sec61 gamma subunit homolog; protein transport to ER.
SEQ ID NO: 667		

AAD51623.1 AF169020 Glycine max
seed maturation protein PM35. PM35. similar to Phaseolus vulgaris putative osmoprotector PvLEA-18.

AAC49859.1 U72764 Phaseolus vulgaris
putative osmoprotector. PvLEA-18. Pvlea-18. atypical late embryogenesis abundant protein.

AAF81194.1 AF240774 Phaseolus vulgaris
LEA-18.

SEQ ID NO: 672

CAB40743.1 AJ011885 Solanum tuberosum
starch branching enzyme II. sbe II.

CAB40746.1 AJ011888 Solanum tuberosum
starch branching enzyme II. SBE II.

CAB40748.1 AJ011890 Solanum tuberosum
starch branching enzyme II. SBE II.

AAD30186.1 AF076679 Triticum aestivum
starch branching enzyme-I. SBE-I.

AAD30187.1 AF076680 Aegilops tauschii
starch branching enzyme-I. SBE-I.

BAA82348.1 AB029548 Phaseolus vulgaris
branching enzyme 1. kbel.

CAA56319.1 X80009 Pisum sativum
starch branching enzyme I. SBEI.

CAB40747.1 AJ011889 Solanum tuberosum
starch branching enzyme II. SBE II.

CAA03846.1 AJ000004 Solanum tuberosum
branches 1,4-alpha glucans. starch branching enzyme II, SBE-II. Sbe-II.

BAA03738.1 D16201 Oryza sativa
branching enzyme-3 precursor.

AAG27623.1 AF286319 Triticum aestivum
starch branching enzyme 2. Sbe2. glucosyltransferase.

CAA72154.1 Y11282 Triticum aestivum
1,4-alpha-glucan branching enzyme II. sbe2.

AAK26821.1 AF338431 Aegilops tauschii
starch branching enzyme IIa. SBEIIa.

AAK26822.1 AF338432 Triticum aestivum
starch branching enzyme IIa variant. SBEIIa variant.

AAC33764.1 AF072725 Zea mays
starch branching enzyme IIb. ae. SBEIIb.

AAA18571.1 L08065 Zea mays
starch branching enzyme II.

BAA82828.1 AB023498 Oryza sativa
starch branching enzyme rbe4. RBE4.

AAC69753.1	AF064560	Hordeum vulgare starch branching enzyme IIa. sbIIa.
CAA56320.1	X80010	Pisum sativum starch branching enzyme II. SBEII.
AAC69754.1	AF064561	Hordeum vulgare starch branching enzyme IIb. sbIIb.
AAC36471.1	AF072724	Zea mays starch branching enzyme I. sbe1. confirmed by partial peptide sequencing.
AAA82735.1	U17897	Zea mays starch branching enzyme I. sbe1.
AAD50279.2	AF169833	Sorghum bicolor seed starch branching enzyme. SBE.
BAA01854.1	D11081	Zea mays branching enzyme-I precursor.
CAA49463.1	X69805	Solanum tuberosum 1,4-alpha-glucan branching enzyme. SBE.
CAA70038.1	Y08786	Solanum tuberosum 1,4-alpha-glucan branching enzyme. sbeI.
AAB17086.1	U66376	Triticum aestivum 1,4-alpha-D-glucan 6-alpha-D-(1,4-alpha-D-glucanotransferase. branching enzyme.
AAB67316.1	U65948	Zea mays formation of alpha-1-6 glucosidic linkage in starch biosynthesis. starch branching enzyme IIa. Sbe2a. starch branching enzyme isozyme SBIIa.
BAB40334.1	AB042937	Ipomoea batatas starch branching enzyme. IBE.
BAA01584.1	D10752	Oryza sativa branching enzyme.
AAD28284.1	AF136268	Oryza sativa subsp. japonica starch-branching enzyme I. Rbe1.
BAA01616.1	D10838	Oryza sativa 1,4-alpha-glucan branching enzyme. sbe1.
BAA01855.1	D11082	Oryza sativa branching enzyme-I precursor.
CAB40981.1	AJ237897	Triticum aestivum starch branching enzyme I. sbe1. alternative.
CAB40979.1	AJ237897	Triticum aestivum starch branching enzyme I. sbe1.
CAB40980.1	AJ237897	Triticum aestivum starch branching enzyme I. sbe1. alternative.
AAG27622.1	AF286318	Triticum aestivum starch branching enzyme 1. Sbe1A. glucosyltransferase.
CAA54308.1	X77012	Manihot esculenta 1,4-alpha-glucan branching enzyme. SBE.

CAA72987.1	Y12320	Triticum aestivum starch branching enzyme I. Sbe1.
AAG27621.1	AF286317	Triticum aestivum starch branching enzyme 1. Sbe1D. glucosyltransferase.
BAA82349.1	AB029549	Phaseolus vulgaris branching enzyme 3. kbe3.
AAB61925.1	AF002820	Triticum aestivum starch branching enzyme I. wSBE I-D2.
CAB40749.1	AJ011891	Solanum tuberosum starch branching enzyme II. SBE II.
CAB40745.1	AJ011887	Solanum tuberosum starch branching enzyme II. SBE II.
CAB40744.1	AJ011886	Solanum tuberosum starch branching enzyme II. SBE II.
BAA85762.1	AB028067	Nicotiana tabacum starch branching enzyme. SBE.
CAA49371.1	X69713	Manihot esculenta branching enzyme. r-2.
BAB40335.1	AB042940	Ipomoea batatas starch branching enzyme. IBE.
CAA49370.1	X69712	Manihot esculenta branching enzyme. r-1.
AAC72336.1	AF064563	Hordeum vulgare starch branching enzyme IIb. sbeIIb.

SEQ ID NO: 673

CAA09881.1	AJ011939	Trifolium repens peroxidase. prx2.
CAA62228.1	X90695	Medicago sativa peroxidase2. prx2.
CAA71495.1	Y10469	Spinacia oleracea peroxidase. prxr8.
AAB41812.1	L36158	Medicago sativa peroxidase. pxdD. amino acid feature: conserved domains, aa 120 .. 126, 188 .. 195; amino acid feature: heme-binding domain, aa 63 .. 68.
BAA77387.1	AB024437	Scutellaria baicalensis peroxidase 1.
AAF63024.1	AF244921	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.
AAD11483.1	U51193	Glycine max peroxidase. sEPb1.
AAB67737.1	L77080	Stylosanthes humilis cationic peroxidase.

BAA07663.1	D42064	Nicotiana tabacum cationic peroxidase isozyme 38K precursor.
BAA07664.1	D42065	Nicotiana tabacum cationic peroxidase isozyme 40K precursor.
CAB94692.1	AJ242742	Ipomoea batatas Removal of H ₂ O ₂ , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
CAB67121.1	Y19023	Lycopersicon esculentum peroxidase. cevi-1.
CAA62226.1	X90693	Medicago sativa peroxidase1B. prx1B.
CAA50597.1	X71593	Lycopersicon esculentum peroxidase. CEVI-1.
AAD11481.1	U51191	Glycine max peroxidase precursor. sEPa1.
AAD11484.1	U51194	Glycine max peroxidase. sEPb2.
BAA82306.1	AB027752	Nicotiana tabacum peroxidase.
AAA65637.1	L13654	Lycopersicon esculentum peroxidase. TPX1.
AAD11482.1	U51192	Glycine max peroxidase precursor. sEPa2.
CAA62225.1	X90692	Medicago sativa peroxidase1A. prx1A.
AAC98519.1	AF007211	Glycine max peroxidase precursor. GMIPER1. pathogen-induced.
AAD37427.1	AF149277	Phaseolus vulgaris peroxidase 1 precursor. FBP1. secretory peroxidase.
BAA14144.1	D90116	Armoracia rusticana peroxidase isozyme.
AAA98491.1	L36981	Petroselinum crispum anionic peroxidase.
CAA71488.1	Y10462	Spinacia oleracea peroxidase. prxr1.
AAD43561.1	AF155124	Gossypium hirsutum bacterial-induced peroxidase precursor. Perx_Goshiko.
BAA14143.1	D90115	Armoracia rusticana peroxidase isozyme.
CAA71490.1	Y10464	Spinacia oleracea peroxidase. prxr3.
AAB02554.1	L37790	Stylosanthes humilis cationic peroxidase.

CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA01877.1	D11102	Populus kitakamiensis peroxidase. prxA1.
CAA62227.1	X90694	Medicago sativa peroxidase1C. prx1C.
BAA07241.1	D38051	Populus kitakamiensis peroxidase. prxA4a.
BAA01950.1	D11337	Vigna angularis peroxidase.
AAF65464.2	AF247700	Oryza sativa peroxidase POC1.
AAF63027.1	AF244924	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
CAC21393.1	AJ401276	Zea mays peroxidase. pox3.
CAA59487.1	X85230	Triticum aestivum peroxidase. pox4.
AAD37430.1	AF149280	Phaseolus vulgaris peroxidase 5 precursor. FBP5. secretory peroxidase.
CAA71491.1	Y10465	Spinacia oleracea peroxidase. prxr4.
AAB41811.1	L36157	Medicago sativa peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.
BAA03644.1	D14997	Oryza sativa peroxidase.
AAA32676.1	M37637	Arachis hypogaea cationic peroxidase. PNC2.
CAA71494.1	Y10468	Spinacia oleracea peroxidase. prxr7.
AAA34050.1	M74103	Nicotiana sylvestris anionic peroxidase.
CAA40796.1	X57564	Armoracia rusticana peroxidase. peroxidase precursor.
SEQ ID NO: 674		
AAG31438.1	AF241793	Perilla frutescens limonene synthase.
BAA08367.1	D49368	Perilla frutescens limonene cyclase.
BAA21629.1	AB005744	Perilla frutescens catalyzing the cyclization of geranyl pyrophosphate to 1-limonene. 1-limonene synthase. gPFLC. similar to perilla PFLC-1:DDBJ Acc#D49368.

AAG31437.1 AF241792	Perilla frutescens limonene synthase.
AAK06663.1 AF317695	Perilla frutescens var. frutescens limonene synthase.
AAG31435.1 AF241790	Perilla citriodora limonene synthase.
AAF65545.1 AF233894	Perilla citriodora limonene synthase.
AAD50304.1 AF175323	Mentha longifolia limonene synthase. monoterpane synthase.
AAC37366.1 L13459	Mentha spicata 4S-limonene synthase.
AAG01140.1 AF282875	Schizonepeta tenuifolia (+)-4R-limonene synthase.
AAC61260.1 AF061285	Capsicum annuum sesquiterpene cyclase. UV induced.
AAG09949.1 AF171216	Lycopersicon esculentum vetispiradiene synthase. LEVS2. sesquiterpene cyclase.
AAF74977.1 AF270425	Gossypium hirsutum (E,E)-farnesyl diphosphate cyclase. (+)-delta-cadinene synthase. cdn2. sesquiterpene cyclase.
BAA82141.1 AB023816	Solanum tuberosum vetispiradiene synthase. PVS4. potato sesquiterpene cyclase.
BAA82092.1 AB022598	Solanum tuberosum vetispiradiene synthase. PVS1. potato sesquiterpene cyclase.
AAF21053.1 AF212433	Capsicum annuum UV-induced sesquiterpene cyclase. SC2.
BAA82109.1 AB022720	Solanum tuberosum vetispiradiene synthase. PVS3. potato sesquiterpene cyclase; PVS3.
BAA82108.1 AB022719	Solanum tuberosum vetispiradiene synthase. PVS2. potato sesquiterpene cyclase; PVS2.
AAC12784.1 U88318	Gossypium hirsutum (E,E)-farnesyl diphosphate cyclizing. (+)-delta-cadinene synthase. cdn1. sesquiterpene cyclase; delta-cadinene synthase.
AAG24640.2 AF304444	Artemisia annua sesquiterpene cyclase.
AAK15641.1 AF326117	Capsicum annuum sesquiterpene cyclase. PSC2.
CAC12731.1 AJ271792	Artemisia annua putative sesquiterpene cyclase. cASC125.
SEQ ID NO: 675	
CAA50609.1 X71609	Nicotiana tabacum ras-related GTP-binding protein.

CAA98166.1	Z73938	Lotus japonicus GTP-binding protein. RAB5A. rab5A.
CAC24477.1	AJ296336	Cichorium intybus x Cichorium endivia GTP binding protein. chi3154.
CAC24476.1	AJ296335	Cichorium intybus x Cichorium endivia GTP binding protein. chi3152.
CAB57220.1	AJ249866	Cichorium intybus x Cichorium endivia GTP binding protein. gtp2.
CAB57219.1	AJ249865	Cichorium intybus x Cichorium endivia GTP binding protein. gtp1.
CAC24475.1	AJ296334	Cichorium intybus x Cichorium endivia GTP binding protein. chi3153.
CAA46112.1	X64941	Nicotiana plumbaginifolia small GTP binding protein.
CAC24474.1	AJ296333	Cichorium intybus x Cichorium endivia GTP binding protein. chi3151.
CAC19792.1	AJ292320	Oryza sativa small GTP-binding protein, RAB family. RAB5A protein. rab5A.
AAD28731.1	AF112964	Triticum aestivum small GTP-binding protein. Sgp.
CAA98167.1	Z73939	Lotus japonicus GTP-binding protein. RAB5B. rab5B.
CAA06922.1	AJ006225	Mesembryanthemum crystallinum small GTP-binding protein. rab5B.
AAG42497.1	AF323991	Oryza sativa small GTP-binding protein RAB5B. rab5B.
BAA84717.1	AB032761	Oryza sativa GTP-binding protein. rab5B.
AAG24438.1	AF304518	Oryza sativa small GTP-binding protein RAB5B. rab5B.
CAB57221.1	AJ249867	Cichorium intybus x Cichorium endivia GTP binding protein. b1.5.
CAA98180.1	Z73952	Lotus japonicus GTP-binding protein. RAB11D. rab11D.
CAA98181.1	Z73953	Lotus japonicus GTP-binding protein. RAB11E. rab11E.
BAA02114.1	D12546	Pisum sativum GTP-binding protein.
BAA02113.1	D12545	Pisum sativum GTP-binding protein.
BAA02116.1	D12548	Pisum sativum GTP-binding protein.

BAA02112.1	D12544	Pisum sativum GTP-binding protein.
BAA02118.1	D12550	Pisum sativum GTP-binding protein.
CAA98159.1	Z73931	Lotus japonicus GTP-binding protein. RAB1B. rab1B.
CAB65172.1	AJ245570	Lycopersicon esculentum putative role in secretion of cell wall modifying enzymes. Rab11 GTPase. Rab11a.
CAA89049.1	Z49190	Beta vulgaris GTP-binding. small G protein.
BAA02110.1	D12542	Pisum sativum GTP-binding protein.
AAB97114.1	U58853	Glycine max small GTP-binding protein. sra1.
BAA02904.1	D13758	Oryza sativa ras-related GTP binding protein. ss230.
CAA98178.1	Z73950	Lotus japonicus GTP-binding protein. RAB11B. rab11B.
CAA98177.1	Z73949	Lotus japonicus GTP-binding protein. RAB11A. rab11A.
AAK15703.1	AF327517	Oryza sativa GTP-binding protein.
AAF65510.1	AF108883	Capsicum annuum small GTP-binding protein.
BAA76422.1	AB024994	Cicer arietinum rab-type small GTP-binding protein.
CAA98160.1	Z73932	Lotus japonicus GTP-binding protein. RAB1C. rab1C.
AAA80680.1	U38466	Lycopersicon esculentum small GTP-binding protein. LeRab1C. ; YPT1/Rab1A homolog LeRab1C.
AAA80678.1	U38464	Lycopersicon esculentum small GTP-binding protein. LeRab1A. ; YPT1/Rab1A homolog LeRab1A.
SEQ ID NO: 676		
AAA80499.1	U20594	Lycopersicon esculentum leucine aminopeptidase.
CAA54314.1	X77015	Solanum tuberosum leucine aminopeptidase. LAP.
CAA48038.1	X67845	Solanum tuberosum leucine aminopeptidase. LAP.
AAC49457.1	U50152	Lycopersicon esculentum peptidase. leucine aminopeptidase. lap2.

AAC49456.1 U50151 Lycopersicon esculentum exoprotease in the defense response. leucine aminopeptidase. lap.

AAA80498.1 U20593 Lycopersicon esculentum leucine aminopeptidase.

CAA68143.1 X99825 Petroselinum crispum cytosol aminopeptidase. leucine aminopeptidase.

BAA90521.1 AB037678 Phaseolus vulgaris leucine aminopeptidase.

SEQ ID NO: 678

CAC09580.1 AJ298992 Fagus sylvatica Abscisic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.

AAA34002.1 M67449 Glycine max protein kinase. PK6.

AAK11734.1 AY027437 Arachis hypogaea serine/threonine/tyrosine kinase.

BAB16918.1 AP002863 Oryza sativa putative protein kinase. P0005A05.22.

CAA06334.1 AJ005077 Lycopersicon esculentum protein kinase. TCTR2 protein. TCTR2.

AAG31141.1 AF305911 Oryza sativa EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.

CAA73722.1 Y13273 Lycopersicon esculentum putative protein kinase.

AAD46406.1 AF096250 Lycopersicon esculentum ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.

AAG31142.1 AF305912 Hordeum vulgare EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.

AAD10056.1 AF110518 Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.

AAD10057.1 AF110519 Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.

AAK30005.1 AY029067 Rosa hybrid cultivar CTR2 protein kinase.

BAB39409.1 AP002901 Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).

BAA87853.1 AP000816 Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

BAA06538.1	D31737	Nicotiana tabacum protein-serine/threonine kinase.
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA94528.1	AP001800	Oryza sativa Similar to Arabidopsis thaliana chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).
BAB17126.1	AP002867	Oryza sativa putative receptor kinase. P0463F06.16.
BAB39451.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.24.
BAB17348.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.32.
BAB17321.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.1.
BAB17129.1	AP002867	Oryza sativa putative receptor kinase. P0463F06.20.
AAF68398.1	AF237568	Oryza sativa receptor-like protein kinase. RLG2.
BAB07905.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.13.
BAA94517.1	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB17335.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.17. contains ESTs D47575(S13157),AU032665(S13157).
BAB39441.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.11.
BAB17116.1	AP002867	Oryza sativa putative receptor kinase. P0463F06.3.
AAF78044.1	AF248493	Oryza sativa receptor-like kinase. RLG18. protein kinase.
CAB51834.1	00069	Oryza sativa I1332.5. contains eukaryotic protein kinase domain PF.
BAB17127.1	AP002867	Oryza sativa putative receptor kinase. P0463F06.17.
AAF78021.1	AF238477	Oryza sativa receptor-like kinase. RLG5. protein kinase.
AAD46420.1	AF100771	Hordeum vulgare receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.
AAD46917.1	AF164021	Oryza sativa receptor kinase.
BAB17345.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.29.

BAB39438.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.7.
AAF78018.1	AF238474	Oryza sativa receptor-like kinase. RLG16. protein kinase.
AAC01746.1	AF044489	Oryza sativa receptor-like protein kinase. drpk1.
BAB17337.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.21. contains ESTs D47575(S13157),AU032665(S13157).
BAB17347.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.31. contains ESTs D47575(S13157),AU032665(S13157).
BAB17344.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.28. contains ESTs D47575(S13157),AU032665(S13157).
BAB39437.1	AP003338	Oryza sativa receptor-like kinase. OJ1212_B09.6.
AAF78019.1	AF238475	Oryza sativa receptor-like kinase. RLG17. protein kinase.
BAA05648.1	D26601	Nicotiana tabacum protein kinase.
BAB17332.1	AP002747	Oryza sativa putative receptor kinase. P0698G03.13. contains ESTs D47575(S13157),AU032665(S13157).
BAB39435.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.2.

SEQ ID NO: 679

CAA78386.1	Z13996	Petunia x hybrida DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
CAB43399.1	AJ006292	Antirrhinum majus Myb-related transcription factor mixta-like 1. mybml1.
CAA67600.1	X99210	Lycopersicon esculentum myb-related transcription factor. THM16.
BAA23337.1	D88617	Oryza sativa transfactor. OSMYB1. Osmyb1.
AAA82943.1	U39448	Picea mariana MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.
CAA64614.1	X95296	Lycopersicon esculentum transcription factor. THM27. myb-related.
BAA93038.1	AP001552	Oryza sativa EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).

AAC04720.1	AF034134	<i>Gossypium hirsutum</i>
putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-O. similar to MYB A encoded by GenBank Accession Number L04497.		
CAA72186.1	Y11351	<i>Oryza sativa</i>
myb factor. myb.		
AAF22256.1	AF161711	<i>Pimpinella brachycarpa</i>
myb-related transcription factor.		
BAB39987.1	AP003020	<i>Oryza sativa</i>
putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).		
BAB39972.1	AP003018	<i>Oryza sativa</i>
putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).		
BAA23338.1	D88618	<i>Oryza sativa</i>
transfactor. OSMYB2. Osmyb2.		
BAA88222.1	AB028650	<i>Nicotiana tabacum</i>
myb-related transcription factor LBM2. lbm2.		
CAA67575.1	X99134	<i>Lycopersicon esculentum</i>
transcription factor. THM6. myb-related.		
CAA78387.1	Z13997	<i>Petunia x hybrida</i>
DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.		
CAA66952.1	X98308	<i>Lycopersicon esculentum</i>
THM18. myb-related transcription factor.		
BAA23339.1	D88619	<i>Oryza sativa</i>
transfactor. OSMYB3. Osmyb3.		
AAC49394.1	U57002	<i>Zea mays</i>
P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.		
AAB41101.1	U72762	<i>Nicotiana tabacum</i>
transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.		
AAA33500.1	M73028	<i>Zea mays</i>
myb-like transcription factor. P.		
AAG36774.1	AF210616	<i>Zea mays</i>
P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.		
BAA88223.1	AB028651	<i>Nicotiana tabacum</i>
myb-related transcription factor LBM3. lbm3.		
BAA88224.1	AB028652	<i>Nicotiana tabacum</i>
myb-related transcription factor LBM4. lbm4.		
CAA72187.1	Y11352	<i>Oryza sativa</i>
myb factor. myb.		

BAA88221.1 AB028649 *Nicotiana tabacum*
myb-related transcription factor LBM1. lbm1.

CAA72185.1 Y11350 *Oryza sativa*
myb factor. myb.

AAG13574.1 AC037425 *Oryza sativa*
myb factor. OSJNBa0055P24.4.

SEQ ID NO: 680

AAA34238.1 L20507 *Vigna radiata*
calmodulin.

AAA34014.1 L01432 *Glycine max*
calcium-binding regulatory protein. calmodulin. SCaM-3. putative.

AAA34013.1 L01430 *Glycine max*
calcium-binding regulatory protein. calmodulin. SCaM-1. putative.

CAA36644.1 X52398 *Medicago sativa*
calmodulin (AA 1-149).

AAD10245.1 AF030033 *Phaseolus vulgaris*
calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.

AAD10244.1 AF030032 *Phaseolus vulgaris*
calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.

CAA74307.1 Y13974 *Zea mays*
calmodulin.

CAA46150.1 X65016 *Oryza sativa*
calmodulin. cam.

AAC36058.1 AF042839 *Oryza sativa*
calmodulin. CaM2.

AAD10246.1 AF030034 *Phaseolus vulgaris*
calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.

CAA54583.1 X77397 *Zea mays*
calmodulin. CaM2.

BAA87825.1 AP000815 *Oryza sativa*
ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene.
Similar to *O.sativa* gene encoding calmodulin. (Z12828).

AAA92681.1 U13882 *Pisum sativum*
calcium-binding protein. calmodulin.

AAA33706.1 M80836 *Petunia x hybrida*
calmodulin. CAM81.

AAA33705.1 M80831 *Petunia x hybrida*
calmodulin-related protein. CAM53.

CAA43143.1 X60738 *Malus x domestica*
Calmodulin. CaM.

CAA78301.1	Z12839	Lilium longiflorum calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	Lilium longiflorum calcium binding protein, signal transduction. calmodulin. putative.
CAA42423.1	X59751	Daucus carota calmodulin. Ccam-1.
CAA67054.1	X98404	Capsicum annuum calmodulin-2. /
AAG27432.1	AF295637	Elaeis guineensis calmodulin.
AAG11418.1	AF292108	Prunus avium calmodulin.
AAA34237.1	L20691	Vigna radiata calmodulin.
AAC49587.1	U49105	Triticum aestivum calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum calmodulin TaCaM3-3. calcium-binding protein.
AAC49585.1	U49103	Triticum aestivum calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum calmodulin TaCaM3-1. calcium-binding protein.
AAC49583.1	U48692	Triticum aestivum calmodulin TaCaM2-3. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum calmodulin TaCaM2-2. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	Triticum aestivum calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	Triticum aestivum calmodulin TaCaM1-1. calcium-binding.
AAA03580.1	L01431	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-2. putative.
AAB36130.1	S81594	Vigna radiata auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.
AAA33901.1	L18913	Oryza sativa calcium binding protein, signal transduction. calmodulin. putative.
CAA78287.1	Z12827	Oryza sativa calcium binding protein, signal transduction. calmodulin.
AAB46588.1	U83402	Capsicum annuum calmodulin.

CAA61980.1	X89890	Bidens pilosa Calmodulin.
AAA32938.1	M27303	Hordeum vulgare calmodulin.
BAA88540.1	AP000969	Oryza sativa ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).
AAF65511.1	AF108889	Capsicum annuum calmodulin.
AAC36059.1	AF042840	Oryza sativa calmodulin. CaM1.
AAA33900.1	L18914	Oryza sativa calcium binding protein, signal transduction. calmodulin.
CAA78288.1	Z12828	Oryza sativa calcium binding protein, signal transduction. calmodulin.
AAA34015.1	L01433	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-4. putative.
AAA16320.1	L14071	Bryonia dioica calmodulin. Bc329. calcium-binding sites (amino acid #): 1. (21..33); 2. (57..68); 3. (94..106); 4. (130..141).
AAA19571.1	U10150	Brassica napus calcium binding. calmodulin. bcml.
AAA87347.1	M88307	Brassica juncea calmodulin.
CAA52602.1	X74490	Zea mays Calmodulin. ZMCALM1.
SEQ ID NO: 683		
CAA71800.1	Y10847	Brassica juncea O-acetylserine(thiol) lyase.
CAA71798.1	Y10845	Brassica juncea O-acetylserine(thiol) lyase.
AAC25635.1	AF044172	Solanum tuberosum cysteine synthase. CS-A; O-acetylserine (thiol) lyase; cytosolic isoform.
BAA01279.1	D10476	Spinacia oleracea O-acetylserine(thiol) lyase.
BAA02438.1	D13153	Triticum aestivum O-acetylserine (thiol) lyase. cys1.
CAA59798.1	X85803	Zea mays O-acetylserine (thiol) lyase. Mcysp. cysteine synthase.
AAD23907.1	AF073695	Oryza sativa cysteine synthase. rcs1. O-acetylserine(thiol)-lyase.
AAD23909.1	AF073697	Oryza sativa cysteine synthase. rcs3. O-acetylserine(thiol)-lyase.

AAC25636.1 AF044173	Solanum tuberosum cysteine synthase. CS-B; O-acetylserine (thiol) lyase; plastidic isoform.
AAC27794.1 AF078693	Chlamydomonas reinhardtii cysteine biosynthesis. putative O-acetylserine(thiol)lyase precursor. Crcys-1A.
CAA06819.1 AJ006024	Cicer arietinum cysteine synthase, O-acetyl-L-serine (thiol)-lyase.
CAA46086.1 X64874	Capsicum annuum O-acetylserine (thiol)-lyase.
CAA71799.1 Y10846	Brassica juncea O-acetylserine(thiol) lyase.
AAA16973.1 L05184	Chloroplast Spinacia oleracea O-acetylserine-(thiol)-lyase.
AAD23908.1 AF073696	Oryza sativa cysteine synthase. rcs2. O-acetylserine(thiol)-lyase.
AAD23910.1 AF073698	Oryza sativa cysteine synthase. rcs4. O-acetylserine(thiol)-lyase.
SEQ ID NO: 684	
AAA68983.1 L12395	Brassica napus signal transduction, membrane vehicle traffic. small GTP-binding protein. bra. putative.
SEQ ID NO: 685	
AAB61961.1 L81152	Oryza sativa integral membrane protein. OsNramp2.
AAB36424.1 S81897	Oryza sativa OsNramp1. OsNramp1. Nramp1 homolog/Bcg product homolog; This sequence comes from Fig. 2.
AAB62273.1 L41217	Oryza sativa integral membrane protein. OsNramp1. putative.
AAC49720.1 U60767	Oryza sativa integral membrane protein OsNramp3. OsNramp3.
SEQ ID NO: 686	
AAC04719.1 AF034133	Gossypium hirsutum putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-N. similar to MYB A encoded by GenBank Accession Number L04497.
AAB58314.1 U33917	Craterostigma plantagineum Cpm7. cpm7. putative DNA-binding protein; myb-like gene; myb-related transcription factor.
AAB58313.1 U33916	Craterostigma plantagineum Cpm5. cpm5. putative DNA-binding protein; myb-related gene; myb-related transcription factor.
AAC13876.1 U33915	Craterostigma plantagineum myb-related transcription factor Cpm10. cpm10. putative DNA-binding protein.

AAK08983.1 AY026332 Oryza sativa

Myb transcription factor JAMyb. related to host cell death and defense responses; induced by jasmonic acid, wounding, or infection of rice blast fungus, but not by salicylic acid or abscisic acid.

BAB18296.1 AP002860 Oryza sativa

putative myb-related transcription factor. P0409B08.23.

CAA71992.1 Y11105 Pisum sativum

Myb26.

BAB40790.1 AB058642 Lilium hybrid division I

LhMyb.

AAK19618.1 AF336285 Gossypium hirsutum

GHMYB38. ghmyb38. similar to myb.

CAA78387.1 Z13997 Petunia x hybrida

DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.

BAA88221.1 AB028649 Nicotiana tabacum

myb-related transcription factor LBM1. lbm1.

BAA88224.1 AB028652 Nicotiana tabacum

myb-related transcription factor LBM4. lbm4.

AAK19617.1 AF336284 Gossypium hirsutum

GHMYB36. ghmyb36. similar to myb.

AAA33067.1 L04497 Gossypium hirsutum

MYB A; putative.

AAK19615.1 AF336282 Gossypium hirsutum

GHMYB10. ghmyb10. similar to myb.

BAA81733.2 AB029162 Glycine max

GmMYB29A2.

BAA81732.1 AB029161 Glycine max

GmMYB29A2.

BAA81730.1 AB029159 Glycine max

GmMYB29A1.

BAA88223.1 AB028651 Nicotiana tabacum

myb-related transcription factor LBM3. lbm3.

AAB41101.1 U72762 Nicotiana tabacum

transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.

BAA81736.1 AB029165 Glycine max

GmMYB29B2.

BAA81731.1 AB029160 Glycine max

GmMYB29A1.

CAA72218.1 Y11415 Oryza sativa

myb.

CAA67000.1	X98355	Oryza sativa activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.
AAK19611.1	AF336278	Gossypium hirsutum BNLGHi233. bnlghi6233. similar to myb.
CAA67575.1	X99134	Lycopersicon esculentum transcription factor. THM6. myb-related.
CAA64614.1	X95296	Lycopersicon esculentum transcription factor. THM27. myb-related.
AAD31395.1	AF114162	Lolium temulentum gibberellin MYB transcription factor. GAMyb. R2/R3-MYB.
BAA93038.1	AP001552	Oryza sativa EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
AAG22863.1	AY008692	Hordeum vulgare transcription factor GAMyb. Gamyb.
BAA96421.1	AB044084	Triticum aestivum transcription activator for gibberellin response. GAMyb protein. Ta-GAMyb.
CAA61021.1	X87690	Hordeum vulgare transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.
CAA66952.1	X98308	Lycopersicon esculentum THM18. myb-related transcription factor.
AAC49394.1	U57002	Zea mays P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.
BAA88222.1	AB028650	Nicotiana tabacum myb-related transcription factor LBM2. lbm2.
AAG36774.1	AF210616	Zea mays P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.
AAA33500.1	M73028	Zea mays myb-like transcription factor. P.
CAC19439.1	AJ237661	Oryza sativa Myb factor protein. myb.
CAB40189.1	AJ133638	Avena sativa transcriptional activator. myb protein. gamyb.
AAK19619.1	AF336286	Gossypium hirsutum GHMYB9. ghmyb9. similar to myb.
AAC04720.1	AF034134	Gossypium hirsutum putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-O. similar to MYB A encoded by GenBank Accession Number L04497.
AAC04716.1	AF034130	Gossypium hirsutum putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-D. similar to MYB A encoded by GenBank Accession Number L04497.

AAG28526.1	AF198499	Nicotiana tabacum anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
CAA78388.1	Z13998	Petunia x hybrida DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.
AAA33482.1	M37153	Zea mays c1 locus myb homologue; putative.
AAK09327.1	AF320614	Zea mays activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
AAK09326.1	AF320613	Zea mays activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
SEQ ID NO: 687		
BAA92972.1	AP001551	Oryza sativa ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).
BAA83689.1	AB011968	Oryza sativa OsPK7. OsPK7. protein kinase.
BAA83688.1	AB011967	Oryza sativa OsPK4. OsPK4. protein kinase.
AAF22219.1	AF141378	Zea mays protein kinase PK4. ZmPK4.
BAA34675.1	AB011670	Triticum aestivum wpk4 protein kinase. wpk4.
CAA73068.1	Y12465	Sorghum bicolor serine/threonine kinase. SNFL2.
CAA73067.1	Y12464	Sorghum bicolor serine/threonine kinase. SNFL1.
BAA92970.1	AP001551	Oryza sativa Similar to Arabidopsis thaliana chromosome 4 BAC clone F28A21 ; putative protein kinase. (AL035526).
CAA74646.1	Y14274	Sorghum bicolor putative serine/threonine protein kinase. SNFL3.
AAD31900.1	AF145482	Mesembryanthemum crystallinum putative serine/threonine protein kinase.
AAB62693.1	AF004947	Oryza sativa protein kinase.
BAA96628.1	AP002482	Oryza sativa ESTs D41739(S4522),AU055999(S20214), AU057588(S21592 correspond to a region of the predicted gene. Similar to Sorghum bicolor serine/threonine kinase (Y12465).

AAD23582.1	AF128443	Glycine max probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.
BAA05649.1	D26602	Nicotiana tabacum protein kinase.
CAA71142.1	Y10036	Cucumis sativus SNF1-related protein kinase.
AAC99329.1	AF062479	Oryza sativa protein kinase SNF1. Snf1. similar to yeast SNF1.
CAA65244.1	X95997	Solanum tuberosum SNF1-related protein kinase. PKIN1.
CAA57898.1	X82548	Hordeum vulgare SNF1-related protein kinase. BKIN2.
CAA07813.1	AJ007990	Hordeum vulgare SnRK1-type protein kinase. kin12a.
CAA46556.1	X65606	Hordeum vulgare protein kinase. BKIN12.
AAB05457.1	U55768	Oryza sativa SNF1-related protein kinase. RSkl. Ser/Thr protein kinase homolog.
CAA46554.1	X65604	Hordeum vulgare protein kinase. BKIN12.
AAD00239.1	U73938	Nicotiana tabacum protein kinase. PK11-C1. PK11-C1. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.
AAC69450.1	AF032465	Nicotiana tabacum putative serine/threonine protein kinase. WAPK.
AAD00240.1	U73939	Nicotiana tabacum protein kinase. PK11-C5. PK11-C5. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.
BAA13608.1	D88399	Oryza sativa serine-threonine kinase. endosperm kinase. REK.
AAA34017.1	L19360	Glycine max protein kinase 2. SPK-2. putative.
AAG60195.1	AC084763	Oryza sativa protein kinase REK. OSJNBa0027P10.6.
AAA33004.1	L12394	Brassica napus serine/threonine protein kination. serine/threonine protein kinase. BSK2. putative.
BAA19573.1	AB002109	Oryza sativa protein kinase. a novel protein kinase.
AAA33979.1	L01453	Glycine max protein phosphorylation, regulatory protein. protein kinase. SPK-1. putative.
AAA33003.1	L12393	Brassica napus protein kination. serine/threonine protein kinase. BSK1. putative.

AAB68962.1	L38855	Glycine max protein kinase. SPK-4.
AAB68961.1	L19361	Glycine max protein kinase 3. SPK-3. putative.
AAB58348.1	U29095	Triticum aestivum serine-threonine protein kinase. TaPK3.
AAF27340.1	AF186020	Vicia faba abscisic acid-activated protein kinase. AAPK.
AAA96325.1	M94726	Triticum aestivum protein kinase. abscisic acid inducible.
CAA81443.1	Z26846	Mesembryanthemum crystallinum protein kinase. MCPK9.
AAG31326.1	AF178575	Vitis vinifera putative serine/threonine kinase GDBrPK. GDBrPK. similar to SNF protein kinase.
CAA06503.1	AJ005373	Craterostigma plantagineum protein kinase. cppk1.
AAF21062.1	AF216527	Dunaliella tertiolecta calcium-dependent protein kinase. CPK1; CDPK.
CAA89202.1	Z49233	Chlamydomonas eugametos calcium-stimulated protein kinase.
SEQ ID NO: 689		
AAC49826.1	U71604	Catharanthus roseus involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.
AAB97311.1	AF008597	Catharanthus roseus desacetoxyvindoline-4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase; involved in the second to last step in vindoline biosynthesis.
AAC49827.1	U71605	Catharanthus roseus involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.
BAA37127.1	AB012203	Lactuca sativa 2-oxoglutarate-dependent dioxygenase. gibberelin 20-oxidase. Ls20ox1.
BAA95828.1	AP002069	Oryza sativa ESTs D47168(S12332),D46350(S10967) correspond to a region of the predicted gene. Similar to Prunus armeniaca ethylene-forming-enzyme-like dioxygenase. (U97530).
AAD56580.1	AF184273	Daucus carota leucoanthocyanidin dioxygenase 1. LDOX1. 2-oxoglutarate dependent dioxygenase.
AAB39995.1	U82432	Dianthus caryophyllus anthocyanidin synthase. allele: S; 2-oxoglutarat-dependent dioxygenase.
AAD56581.1	AF184274	Daucus carota leucoanthocyanidin dioxygenase 2. LDOX. 2-oxoglutarate dependent dioxygenase.
SEQ ID NO: 691		

AAA34002.1	M67449	Glycine max protein kinase. PK6.
CAC09580.1	AJ298992	Fagus sylvatica Abscisic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.
AAK11734.1	AY027437	Arachis hypogaea serine/threonine/tyrosine kinase.
BAB16918.1	AP002863	Oryza sativa putative protein kinase. P0005A05.22.
CAA06334.1	AJ005077	Lycopersicon esculentum protein kinase. TCTR2 protein. TCTR2.
AAD10057.1	AF110519	Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.
AAD10056.1	AF110518	Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.
CAA73722.1	Y13273	Lycopersicon esculentum putative protein kinase.
AAD46406.1	AF096250	Lycopersicon esculentum ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.
AAG31141.1	AF305911	Oryza sativa EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAG31142.1	AF305912	Hordeum vulgare EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAK30005.1	AY029067	Rosa hybrid cultivar CTR2 protein kinase.
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAF91323.1	AF244889	Glycine max receptor-like protein kinase 2. RLK2. GmRLK2.
AAF91324.1	AF244890	Glycine max receptor-like protein kinase 3. RLK3. GmRLK3.
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAF91322.1	AF244888	Glycine max receptor-like protein kinase 1. RLK1. GmRLK1.

BAB18292.1	AP002860	Oryza sativa putative receptor-like protein kinase. P0409B08.19.
AAK16409.1	AF320086	Zea mays serine threonine kinase 1. stk1. expressed in mature tassel.
BAA06538.1	D31737	Nicotiana tabacum protein-serine/threonine kinase.
BAA21132.1	D88193	Brassica rapa S-receptor kinase. SRK9 (B.c.).
BAA06285.1	D30049	Brassica rapa S-receptor kinase SRK9.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
CAB54520.1	AJ238845	Brassica napus putative role in cell cycle control. MAP3K epsilon 1 protein kinase. MAP3Ke1.
CAA97692.1	Z73295	Catharanthus roseus receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
CAA08995.1	AJ010091	Brassica napus MAP3K alpha 1 protein kinase. MAP3K alpha 1.
BAB40094.1	AP003210	Oryza sativa putative receptor protein kinase. OSJNBa0010K01.7.
CAB51834.1	00069	Oryza sativa l1332.5. contains eukaryotic protein kinase domain PF.
BAB40021.1	AP003021	Oryza sativa putative wall-associated kinase 2. P0503E05.25. contains EST C24950(S16264).
AAF43496.1	AF131222	Lophopyrum elongatum protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	Lophopyrum elongatum protein kinase. ESI47.
AAA62232.1	U00443	Brassica napus S-receptor kinase. protein contains an immunoglobulin-like domain.
BAB40010.1	AP003021	Oryza sativa putative wall-associated kinase 2. P0503E05.12.
AAC36318.1	AF053127	Malus x domestica leucine-rich receptor-like protein kinase. LRPKm1.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
BAB18321.1	AP002865	Oryza sativa putative receptor protein kinase. P0034C11.11.

BAA92836.1 AB032473 *Brassica oleracea*
S18 S-locus receptor kinase. SRK18.

AAA33915.1 L27821 *Oryza sativa*
receptor type serine/threonine kinase. protein kinase.

BAB40081.1 AP003074 *Oryza sativa*
putative receptor protein kinase. OSJNBa0004G10.30.

AAD38286.1 AC007789 *Oryza sativa*
putative protein kinase. OSJNBa0049B20.13.

BAA92837.1 AB032474 *Brassica oleracea*
S60 S-locus receptor kinase. SRK60.

SEQ ID NO: 692

AAK16172.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.14.

AAF17077.1 AF199453 *Sorghum bicolor*
UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.

AAF61647.1 AF190634 *Nicotiana tabacum*
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA89009.1 AB027455 *Petunia x hybrida*
anthocyanin 5-O-glucosyltransferase. PH1.

AAF98390.1 AF287143 *Brassica napus*
catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeoate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

AAD21086.1 AF127218 *Forsythia x intermedia*
adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.

BAA93039.1 AB033758 *Citrus unshiu*
limonoid UDP-glucosyltransferase. LGTase.

BAA83484.1 AB031274 *Scutellaria baicalensis*
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

BAA12737.1 D85186 *Gentiana triflora*
UDP-glucose:flavonoid-3-glucosyltransferase.

CAA54612.1 X77462 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT5.

BAA19155.1 AB000623 *Nicotiana tabacum*
glucosyl transferase. JIGT.

BAA89008.1 AB027454 *Petunia x hybrida*
anthocyanidin 3-O-glucosyltransferase. PGT8.

BAB17060.1 AP002523 *Oryza sativa*
putative glucosyl transferase. P0013F10.6.

BAA90787.1 AB038248 *Ipomoea batatas*
UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.

AAK16178.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.5.
AAK16175.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.15.
AAB36653.1	U32644	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS5a.
AAB36652.1	U32643	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28303.1	AF346431	Nicotiana tabacum phenylpropanoid:glucosyltransferase 1. tog1. glucosyltransferase.
AAK28304.1	AF346432	Nicotiana tabacum phenylpropanoid:glucosyltransferase 2. tog2. glucosyltransferase.
BAB17061.1	AP002523	Oryza sativa putative glucosyl transferase. P0013F10.7. contains EST C73149(E2992).
CAA30761.1	X07940	Zea mays UDPGlucose flavonoid glycosyl-transferase. Bz-McC.
AAK16410.1	AF320086	Zea mays UDPG-flavonoid 3-O-glucosyl transferase. bz.
CAA31855.1	X13500	Zea mays UDPGlucose:flavonol 3-O-glucosyltransferase.
BAB17059.1	AP002523	Oryza sativa putative glucosyl transferase. P0013F10.5.
BAA36421.1	AB013596	Perilla frutescens UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.
AAB86473.1	AF028237	Ipomoea purpurea UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
CAA30760.1	X07937	Zea mays UDPGlucose flavonoid glycosyl transferase. Bz-W22.
BAB41021.1	AB047094	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAB41019.1	AB047092	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41025.1	AB047098	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
AAD55985.1	AF165148	Petunia x hybrida catalyzes the penultimate step of flavonol glucosylgalactoside biosynthesis from UDP-galactose and flavonol aglycones in petunia pollen. UDP-galactose:flavonol 3-O-galactosyltransferase. F3galtase.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.

BAB41017.1 AB047090	Vitis labrusca x Vitis vinifera
UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.	
AAK16181.1 AC079887	Oryza sativa
putative glucosyltransferase. OSJNBA0040E01.16.	
BAB41023.1 AB047096	Vitis vinifera
UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT1.	
CAA59450.1 X85138	Lycopersicon esculentum
twi1, homologous to glucosyltransferases.	
CAA54614.1 X77464	Manihot esculenta
UTP-glucose glucosyltransferase. CGT7.	
AAB81682.1 AF000371	Vitis vinifera
UDP glucose:flavonoid 3-o-glucosyltransferase.	
AAB81683.1 AF000372	Vitis vinifera
UDP glucose:flavonoid 3-o-glucosyltransferase.	
BAB41024.1 AB047097	Vitis vinifera
UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT2.	
CAA54558.1 X77369	Solanum melongena
glycosyl transferase. GT.	
BAB41026.1 AB047099	Vitis vinifera
UDP-glucose:flavonoid 3-O-glucosyltransferase. FlUFGT2.	
BAB41020.1 AB047093	Vitis vinifera
UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.	
BAB41022.1 AB047095	Vitis vinifera
UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.	
BAA19659.1 AB002818	Perilla frutescens
flavonoid 3-O-glucosyltransferase. UDP glucose.	
AAG25643.1 AF303396	Phaseolus vulgaris
UDP-glucosyltransferase HRA25. putative; defense associated.	
SEQ ID NO: 694	
BAB40923.1 AB059401	Oryza sativa
putative selenium binding protein. Os SBP.	
SEQ ID NO: 695	
AAD26942.1 AF119050	Datisca glomerata
zinc-finger protein 1. zfp1. DgZFP1.	
BAA05079.1 D26086	Petunia x hybrida
zinc-finger protein.	
AAB39638.1 U68763	Glycine max
putative transcription factor. SCOF-1. scof-1. zinc-finger protein.	
CAB77055.1 Y18788	Medicago sativa
putative TFIIIA (or kruppel)-like zinc finger protein.	
AAC06243.1 AF053077	Nicotiana tabacum
transcription factor. osmotic stress-induced zinc-finger protein. zfp.	

BAA05077.1	D26084	Petunia x hybrida zinc-finger DNA binding protein.
BAA05076.1	D26083	Petunia x hybrida zinc-finger DNA binding protein.
AAB53260.1	U76554	Brassica rapa transcription factor. zinc-finger protein-1. BR42.
BAA05078.1	D26085	Petunia x hybrida zinc-finger DNA binding protein.
AAB53261.1	U76555	Brassica rapa zinc-finger protein BcZFP1. BcZFP1(3-2z).
AAK01713.1	AF332876	Oryza sativa zinc finger transcription factor ZF1.
BAA21920.1	AB006598	Petunia x hybrida ZPT2-11. C2H2 zinc finger protein, 2finger.
BAA21922.1	AB006600	Petunia x hybrida ZPT2-13. C2H2 zinc finger protein, 2finger.
BAA19112.1	AB000453	Petunia x hybrida PEThy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.
BAA21927.1	AB006605	Petunia x hybrida ZPT3-3. C2H2 zinc finger protein, 3 finger.
BAA96071.1	AB035133	Petunia x hybrida C2H2 zinc-finger protein ZPT3-3. ZPT3-3.
BAA96070.1	AB035132	Petunia x hybrida C2H2 zinc-finger protein ZPT2-10. PEThy;ZPT2-10.
BAA21919.1	AB006597	Petunia x hybrida ZPT2-10. C2H2 zinc finger protein, 2 finger.
BAA19114.1	AB000455	Petunia x hybrida PEThy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.
BAA21921.1	AB006599	Petunia x hybrida ZPT2-12. C2H2 zinc finger protein, 2 finger.
BAA21928.1	AB006606	Petunia x hybrida ZPT4-4. C2H2 zinc finger protein, 4 finger.
CAA60828.1	X87374	Pisum sativum putative zinc finger protein.
BAA21925.1	AB006603	Petunia x hybrida ZPT2-8. C2H2 zinc finger protein, 2 finger.
BAA19111.1	AB000452	Petunia x hybrida PEThy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.
BAA19926.1	AB000456	Petunia x hybrida PEThy; ZPT4-2. C2H2 zinc finger protein, 4 finger.
BAA21924.1	AB006602	Petunia x hybrida ZPT2-7. C2H2 zinc finger protein, 2finger.

BAA21923.1 AB006601	Petunia x hybrida
ZPT2-14. C2H2 zinc finger protein, 2 finger.	
BAA21926.1 AB006604	Petunia x hybrida
ZPT2-9. C2H2 zinc finger protein, 2 finger.	
BAA19110.1 AB000451	Petunia x hybrida
PEThy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.	
BAA19113.1 AB000454	Petunia x hybrida
PEThy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.	
SEQ ID NO: 702	
AAC29419.1 AF348319	Zea mays
TERMINAL EAR1. tel1. RNA-binding protein; 3 putative RRM motifs; similar to Schizosaccharomyces pombe Mei2 and Arabidopsis AML1; tel1 cDNA sequence is presented in GenBank Accession Number AF047852.	
CAA57551.1 X82030	Phaseolus vulgaris
chloroplast RNA binding protein. RNP1.	
CAA66479.1 X97905	Vicia faba
RNA- or ssDNA-binding protein.	
CAC01237.1 AJ292767	Nicotiana plumbaginifolia
nuclear RNA binding protein. RNA Binding Protein 45. rbp45.	
AAF66823.1 AF190655	Nicotiana tabacum
poly(A)-binding protein. PABP.	
AAK30205.1 AF349964	Daucus carota
poly(A)-binding protein. Translin1P.	
AAG59664.1 AC084319	Oryza sativa
putative RNA binding protein. OSJNBA0004B24.1.	
AAB38974.1 U81318	Triticum aestivum
poly(A)-binding protein. wheatpab.	
CAA81127.1 Z26042	Anemia phyllitidis
Binding to the poly(A)-tail of eukaryotic mRNAs. poly(A)-mRNA binding protein.	
AAA79045.1 U34742	Spinacia oleracea
24 kDa RNA binding protein.	
AAC39368.1 AF043297	Chlamydomonas reinhardtii
poly(A) binding protein RB47. PABP.	
AAF63202.1 AF240679	Cucumis sativus
poly(A)-binding protein.	
CAA11894.1 AJ224325	Hordeum vulgare
nucleic acid-binding protein. cp33Hv.	
AAF66825.1 AF190657	Nicotiana tabacum
poly(A)-binding protein. PABP.	
CAA06469.1 AJ005286	Hordeum vulgare
nucleic acid-binding protein. cp31AHv protein.	
SEQ ID NO: 709	

AAB36546.1 U77940 *Phaseolus vulgaris*
polyubiquitin. expression is regulated by heavy metal stress, UV, virus infection, heat shock
and wounding treatment, this suggests that ubiquitin plays a role in plant defense.

SEQ ID NO: 714

CAA61946.1 X89828 *Pisum sativum*
fructose-1,6-bisphosphate aldolase.

AAB61592.1 AF003124 *Mesembryanthemum crystallinum*
fructose-biphosphate aldolase.

CAB77243.2 AJ133146 *Persea americana*
glycolytic enzyme, sixth step in glycolysis. fructose-bisphosphate aldolase. alf.

BAA08845.1 D50307 *Oryza sativa*
aldolase C-1.

BAA08830.1 D50301 *Oryza sativa*
aldolase C-1.

CAA46649.1 X65742 *Spinacia oleracea*
fructose-bisphosphate aldolase.

BAA02729.1 D13512 *Oryza sativa*
cytoplasmic aldolase.

AAG21429.1 AF308587 *Fragaria x ananassa*
cytosolic aldolase. SCA1.

CAA37290.1 X53130 *Oryza sativa*
fructose-diphosphate aldolase (AA 1-358).

CAA31366.1 X12872 *Zea mays*
fructose bisphosphate aldolase.

AAA33435.1 M16220 *Zea mays*
aldolase.

CAA61947.1 X89829 *Pisum sativum*
fructose-1,6-bisphosphate aldolase.

CAA06308.1 AJ005041 *Cicer arietinum*
cytosolic fructose-1,6-bisphosphate aldolase.

AAK19324.1 AF329673 *Dunaliella salina*
fructose-bisphosphate aldolase isoenzyme 1. salt-induced.

CAA71408.1 Y10380 *Solanum tuberosum*
homologous to plastidic aldolases.

BAA77603.1 AB027002 *Nicotiana paniculata*
plastidic aldolase.

BAA77604.1 AB027001 *Nicotiana paniculata*
plastidic aldolase NPALDP1. NpAldP1.

AAA33642.1 M97476 *Pisum sativum*
aldolase.

AAA33643.1 M97477 *Pisum sativum*
aldolase.

BAA02730.1	D13513	Oryza sativa chloroplastic aldolase.
AAF74220.1	AF216582	Avena sativa fructose 1,6-bisphosphate aldolase precursor.
CAA47293.1	X66814	Spinacia oleracea fructose-bisphosphate aldolase.
AAK19325.1	AF329674	Dunaliella salina fructose-bisphosphate aldolase isoenzyme 2. salt-induced.
CAB46520.1	AJ243524	Phleum pratense sixth step in glycolysis. putative fructose-bisphosphate aldolase.
CAA09669.1	AJ011516	Scherffelia dubia fructose-bisphosphate aldolase.
CAA49590.1	X69969	Chlamydomonas reinhardtii fructose-bisphosphate aldolase. ALDCHL.
AAC60574.1	S72951	Chloroplast Chlamydomonas reinhardtii fructosediphosphate aldolase. fructosediphosphate aldolase. This sequence comes from Fig. 4.
AAB70542.1	AF017362	Oryza sativa aldolase.
BAA76430.1	AB025002	Cicer arietinum fructose-bisphosphate aldolase.
AAD20818.1	AF107590	Dendrobium grex Madame Thong-In putative fructose-bisphosphate aldolase. otg11.
BAA11395.1	D78500	Brassica rapa putative aldolase. Sequence homologous to cytoplasmic aldolase of rice (D13512).
BAA78593.1	AU066535	Chlamydomonas sp. HS-5 fructose-bisphosphate aldolase precursor. NaCl inducible.
CAC34412.1	Y18576	Flaveria trinervia fructose-bisphosphate aldolase. alf.

SEQ ID NO: 715

AAK07429.1	AF321287	Musa acuminata beta-glucosidase.
AAC69619.1	AF072736	Pinus contorta beta-glucosidase.
AAF04007.1	AF163097	Dalbergia cochinchinensis beta-fucosidase beta-glucosidase. dalcochinin 8'-O-beta-glucoside beta-glucosidase precursor. BGLU1. rotenoid beta-glucosidase.
AAA93032.1	U50201	Prunus serotina hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase precursor. located in protein bodies of Prunus seeds; encodes 8 putative N-glycosylation sites (N-X-S/T); encodes NEP and ITENG motifs characteristic of the BGA family of beta-glucosidases.
BAA78708.1	AB003089	Polygonum tinctorium beta-glucosidase.

AAA91166.1	U39228	<i>Prunus avium</i> beta-glucosidase.
BAA11831.1	D83177	<i>Costus speciosus</i> saponin metabolite. furostanol glycoside 26-O-beta-glucosidase (F26G). functional expression in <i>E. coli</i> ; one of the F26G isoforms.
AAF34650.1	AF221526	<i>Prunus serotina</i> hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase isoform PHA precursor. beta-glucosidase; contains 6 potential N-glycosylation sites (N-X-S/T); glycosyl hydrolase family 1 member.
AAG25897.1	AF170087	<i>Cucurbita pepo</i> silverleaf whitefly-induced protein 3. SLW3. similar to beta-glucosidase.
AAG00614.1	AF293849	<i>Secale cereale</i> beta-glucosidase.
AAB22162.1	S35175	<i>Manihot esculenta</i> linamarase. linamarase. beta-glucosidase; Method: conceptual translation with partial peptide sequencing; This sequence comes from Fig. 4.
AAF03675.1	AF149311	<i>Rauvolfia serpentina</i> hydrolyses the glucoalkaloid raucaffricine. raucaffricine-O-beta-D-glucosidase. beta glucosidase; RG; part of the Ajmaline biosynthesis pathway; belongs to family 1 of the glucosyl hydrolases.
AAA87339.1	L41869	<i>Hordeum vulgare</i> beta-glucosidase. BGQ60. expression specific to starchy endosperm of seed.
AAC49177.1	U33817	<i>Sorghum bicolor</i> beta-glucosidase, catalyzes the hydrolysis of the cyanogenic beta-glucoside dhurrin. dhurrinase.
CAA64442.1	X94986	<i>Manihot esculenta</i> beta glucosidase. bglA.
AAD02839.1	AF082991	<i>Avena sativa</i> beta-D-glucosidase beta subunit precursor. P60b. avenacosidase.
AAD09850.1	U44087	<i>Zea mays</i> beta-D-glucosidase precursor. glu2. product subunit structure: autodimer of 58.4 kDa monomers Allele: glu2-B73.
AAD10503.1	U33816	<i>Zea mays</i> functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
AAB03266.1	U44773	<i>Zea mays</i> beta-D-glucosidase. glu1. autodimer of 58.4 kD monomers.
AAA65946.1	U25157	<i>Zea mays</i> functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
CAA52293.1	X74217	<i>Zea mays</i> beta-glucosidase. p60.1.

AAF28800.1 AF112888	<i>Catharanthus roseus</i>	plays a role in secondary metabolism by hydrolyzing strictosidine to cathenamine during indole alkaloid biosynthesis. strictosidine beta-glucosidase. localized in the endoplasmic reticulum.
CAA40057.1 X56733	<i>Trifolium repens</i>	beta-glucosidase. Li.
CAA40058.1 X56734	<i>Trifolium repens</i>	beta-glucosidase. non-cyanogenic.
CAA55196.1 X78433	<i>Avena sativa</i>	beta-D-glucosidase.
CAA79989.2 Z21977	<i>Brassica napus</i>	beta thioglucosidase. myrosinase, thioglucoside glucohydrolase. Myr1.Bn1.
AAB71381.1 U95298	<i>Manihot esculenta</i>	linamarase. pLIN-GEN. beta-glucosidase.
CAA57913.1 X82577	<i>Brassica napus</i>	beta-glucosidase. bgl.
AAB38784.1 U72154	<i>Brassica nigra</i>	beta-glucosidase. psr3.1. PSR3.1; phosphate-starvation responsive enzyme.
AAF34651.1 AF221527	<i>Prunus serotina</i>	putative prunasin hydrolase precursor. beta-glucosidase; glycosyl hydrolase family 1 member.
AAA84906.1 U28047	<i>Oryza sativa</i>	catalyzes the release of either gibberellin or cyanogenic substances from their glucoconjugates. beta glucosidase. beta-D-glucoside glucohydrolase; dimer of 60 kDa monomers; localized in the plastid.
CAC08209.1 AJ005950	<i>Cicer arietinum</i>	beta-glucosidase.
SEQ ID NO: 718		
AAF61647.1 AF190634	<i>Nicotiana tabacum</i>	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA89009.1 AB027455	<i>Petunia x hybrida</i>	anthocyanin 5-O-glucosyltransferase. PH1.
BAA93039.1 AB033758	<i>Citrus unshiu</i>	limonoid UDP-glucosyltransferase. LGTase.
BAA36423.1 AB013598	<i>Verbena x hybrida</i>	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
BAA36421.1 AB013596	<i>Perilla frutescens</i>	UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.
AAF98390.1 AF287143	<i>Brassica napus</i>	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
BAA36422.1 AB013597	<i>Perilla frutescens</i>	UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.

BAB07962.1	AP002524	Oryza sativa putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481), AU067882(C10481).
AAD21086.1	AF127218	Forsythia x intermedia adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
AAK16178.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.5.
BAA12737.1	D85186	Gentiana triflora UDP-glucose:flavonoid-3-glucosyltransferase.
AAK16181.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.16.
AAK16175.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.15.
AAK16172.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.14.
CAA59450.1	X85138	Lycopersicon esculentum tw1. homologous to glucosyltransferases.
AAF17077.1	AF199453	Sorghum bicolor UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
BAA89008.1	AB027454	Petunia x hybrida anthocyanidin 3-O-glucosyltransferase. PGT8.
AAB81683.1	AF000372	Vitis vinifera UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
AAB81682.1	AF000371	Vitis vinifera UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41022.1	AB047095	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41020.1	AB047093	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAB41021.1	AB047094	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAB41019.1	AB047092	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAA83484.1	AB031274	Scutellaria baicalensis UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
BAB41025.1	AB047098	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

BAB41023.1 AB047096	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. A1UFGT1.
BAA90787.1 AB038248	Ipomoea batatas UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.
BAA19659.1 AB002818	Perilla frutescens flavonoid 3-O-glucosyltransferase. UDP glucose.
BAB41018.1 AB047091	Vitis labrusca x Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.
AAB36652.1 U32643	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1 AF346432	Nicotiana tabacum phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
BAB41024.1 AB047097	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. A1UFGT2.
BAB41026.1 AB047099	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
CAA31855.1 X13500	Zea mays UDPGlucose:flavonol 3-O-glucosyltransferase.
AAB86473.1 AF028237	Ipomoea purpurea UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
CAA54614.1 X77464	Manihot esculenta UTP-glucose glucosyltransferase. CGT7.
SEQ ID NO: 719	
AAC24195.1 AF020425	Nicotiana tabacum calmodulin binding protein. glutamate decarboxylase isozyme 1. NtGAD1. calcium-calmodulin-dependent enzyme.
AAK18620.1 AF352732	Nicotiana tabacum converts glutamate to gamma-aminobutyric acid. glutamate decarboxylase isozyme 3. GAD; GAD3; NtGAD3; calcium/calmodulin-dependent enzyme.
AAB40608.1 U54774	Nicotiana tabacum glutamate decarboxylase. NtGAD1. calmodulin regulated enzyme; calmodulin-binding protein.
AAA33710.1 L16977	Petunia x hybrida glutamate decarboxylase. gad.
AAA33709.1 L16797	Petunia x hybrida glutamate decarboxylase. gad.
AAC39483.1 AF020424	Nicotiana tabacum glutamate decarboxylase isozyme 2. NtGAD2. calcium-calmodulin-dependent enzyme.
BAB32870.1 AB056062	Oryza sativa glutamate decarboxylase. GAD.
BAB32868.1 AB056060	Oryza sativa glutamate decarboxylase. GAD.

CAA56812.1 X80840 *Lycopersicon esculentum*
homology to pyridoxal-5'-phosphate-dependant glutamate decarboxylases; putative start codon.

BAB32871.1 AB056063 *Oryza sativa*
glutamate decarboxylase. GAD.

BAB32869.1 AB056061 *Oryza sativa*
glutamate decarboxylase. GAD.

CAA50719.1 X71900 *Lycopersicon esculentum*
histidine decarboxylase. hdc. pyridoxal 5'-phosphate dependant.

SEQ ID NO: 720

BAA92713.1 AP001389 *Oryza sativa*
ESTs AU033035(S1515),D39871(S1515) correspond to a region of the predicted gene.
Similar to *Arabidopsis thaliana* chromosome II BAC F22D22 genomic sequence; putative glucan synthase (AC006223).

AAD25952.1 AF085717 *Gossypium hirsutum*
putative callose synthase catalytic subunit. CFL1. cotton FKS1-like protein; similar to *Saccharomyces cerevisiae* beta-1,3-glucan synthase subunit FKS1.

SEQ ID NO: 721

CAB55396.1 AL117264 *Oryza sativa*
zwh12.1. similar to *Arabidopsis* putative UDP-galactose-4-epimerase (AC007060); Method:
conceptual translation with partial peptide sequencing.

CAA06339.1 AJ005082 *Cyamopsis tetragonoloba*
UDP-galactose 4-epimerase.

AAA86532.1 U31544 *Pisum sativum*
catabolism of galactose to glucose in Leloir pathway, and in galactose synthesis from glucose.
UDP-galactose-4-epimerase. galE. galactowaldenase.

CAA06338.1 AJ005081 *Cyamopsis tetragonoloba*
UDP-galactose 4-epimerase.

BAB40967.1 AB059568 *Pisum sativum*
biosynthesis of UDP-D-xylose. UDP-D-glucuronate carboxy-lyase. uxs1.

SEQ ID NO: 726

BAA88198.1 AP000837 *Oryza sativa*
Similar to human dimethylaniline monooxygenase (AC002376).

BAA35120.1 AB008845 *Oryza sativa*
NADH dependent Glutamate Synthase.

AAB41904.1 L37606 *Medicago sativa*
NADH-dependent glutamate synthase.

BAA88195.1 AP000837 *Oryza sativa*
Similar to human dimethylaniline monooxygenase (AC002376).

AAB46617.1 L01660 *Medicago sativa*

the 3 cysteine residues in this region (amino acid residues 1246-1257) may serve to coordinate the [3Fe-4S] cluster that is probably found in this protein. See Knaff et al. (1991) J. Biol. Chem. 266:150. NADH-glutamate synthase. NADH-GOGAT; activity increases dramatically during nodule development; the 3 cysteine residues in this region may serve to coordinate the [3Fe-4S] cluster that is probably found in this protein. See Knaff et al. (1991) J. Biol. Chem. 266:15080-15084.

SEQ ID NO: 728

AAG43550.1 AF211532 *Nicotiana tabacum*

Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.

BAA96875.1 AB045121 *Oryza sativa*

RING finger 1. RRF1.

AAK00436.1 AC060755 *Oryza sativa*

putative zinc finger protein. OSJNBa0003O19.23.

BAA78746.1 AB023482 *Oryza sativa*

Similar to Arabidopsis thaliana RING-H2 finger protein RHX1a mRNA, partial cds. (AF079184).

CAA74911.1 Y14573 *Hordeum vulgare*

ring finger protein. putative.

AAG46117.1 AC073166 *Oryza sativa*

putative ring finger protein. OSJNBb0064P21.7.

BAA85438.1 AP000616 *Oryza sativa*

similar to RING-H2 finger protein RHA1a (AF078683).

BAA77204.1 AB026262 *Cicer arietinum*

ring finger protein.

SEQ ID NO: 730

AAA86424.1 U44386 *Lycopersicon esculentum*

heat shock protein. TFHS1. similar to protein encoded by the arg2 gene in mung bean, encoded by Genbank Accession Number D14411.

SEQ ID NO: 731

CAA06756.1 AJ005899 *Nicotiana tabacum*

G subunit. G subunit of Vacuolar-type H⁺-ATPase. vag1.

CAA06757.1 AJ005900 *Nicotiana tabacum*

Subunit G of vacuolar-type H⁺-ATPase. vag2. vag2.

AAD56039.1 AF184068 *Citrus limon*

vacuolar membrane ATPase subunit G. LVMA10. V-ATPase VMA10.

SEQ ID NO: 737

AAF69008.1 AF257779 *Oryza sativa*

stress-inducible protein. OsSI1.

SEQ ID NO: 739

CAC12996.1 AJ299398 *Medicago truncatula*

putative auxin import. putative AUX1-like permease. lax2.

AAF21982.1 AF115543 Populus tremula x Populus tremuloides
AUX1-like protein. PAX1.

AAG17171.1 AF190880 Populus tremula x Populus tremuloides
putative AUX1-like permease. pax5.

CAC12995.1 AJ299397 Medicago truncatula
putative auxin import. putative AUX1-like permease. lax1.

CAC12997.1 AJ299399 Medicago truncatula
putative auxin import. putative AUX1-like permease. lax3.

CAB65535.1 AJ0111794 Zea mays
AUX1 protein. aux1.

SEQ ID NO: 740

CAA65269.1 X96406 Solanum tuberosum
13-lipoxygenase.

AAB65767.1 U37840 Lycopersicon esculentum
lipoxygenase. loxD. wound, systemin and methyl-jasmonate induced.

BAA03102.1 D14000 Oryza sativa
lipoxygenase. lox2osPil.

AAC12951.1 U56406 Hordeum vulgare
methyljasmonate-inducible lipoxygenase 2.

CAB94852.1 AJ404331 Prunus dulcis
hydroperoxydation of polyunsaturated fatty acids. lipoxygenase. lox.

AAG21691.1 AY008278 Lycopersicon esculentum
lipoxygenase. oxido-reductase.

AAA79186.1 U36339 Cucumis sativus
lipoxygenase.

AAB67858.1 U60200 Solanum tuberosum
lipoxygenase. POTLX-1. expressed during early tuberization.

CAA64765.1 X95512 Solanum tuberosum
lipoxygenase.

CAB83038.1 AJ271161 Cucumis sativus
oxygenase. lipoxygenase-9. lox9.

CAA58859.1 X84040 Nicotiana tabacum
lipoxygenase. Lox1.

AAB67865.1 U60202 Solanum tuberosum
lipoxygenase. POTLX-3. expressed in ABA-treated leaves.

CAA55724.1 X79107 Solanum tuberosum
lipoxygenase. Lox1:St:1.

AAB67860.1 U60201 Solanum tuberosum
lipoxygenase. POTLX-2. expressed during early tuberization.

CAB65460.1 Y18548 Solanum tuberosum
lipoxygenase. lox1-St-2.

AAD04258.1	AF039651	Solanum tuberosum 5-lipoxygenase.
AAB81594.1	AF019613	Solanum tuberosum lipoxygenase. plox1.
AAA33986.1	J02795	Glycine max lipoxygenase-1.
AAB67732.1	U50075	Glycine max lipoxygenase L-5. vlxB.
CAA47717.1	X67304	Glycine max lipoxygenase.
AAB81595.1	AF019614	Solanum tuberosum lipoxygenase. plox2.
CAA64766.1	X95513	Solanum tuberosum lipoxygenase.
AAB31252.1	S73865	Solanum tuberosum linoleate:oxygen oxidoreductase. linoleate:oxygen oxidoreductase, lipoxygenase, LOX. This sequence comes from Fig. 1; lipoxygenase; LOX.
AAA53184.1	U09026	Lycopersicon esculentum lipoxygenase. loxA.
AAB65766.1	U37839	Lycopersicon esculentum lipoxygenase. loxC. expressed during ripening fruit.
CAA65268.1	X96405	Solanum tuberosum 13-lipoxygenase.
AAF15296.2	AF204210	Phaseolus vulgaris lipoxygenase. LOX4.
CAA55319.1	X78581	Pisum sativum lipoxygenase. Lox1:Ps:3.
AAA03728.1	U04526	Glycine max lipoxygenase.
CAA34906.1	X17061	Pisum sativum lipoxygenase (AA 1-864).
CAA55318.1	X78580	Pisum sativum lipoxygenase. Lox1:Ps:2.
BAA03042.1	D13949	Glycine max lacking. lipoxygenase-2. lox2.
AAA33987.1	J03211	Glycine max lipoxygenase (EC 1.13.11.12).
AAB71759.1	U84198	Pisum sativum lipoxygenase. Lox1:Ps:1. expressed in root nodules.
AAB41272.1	U50081	Glycine max lipoxygenase-3.
CAA39604.1	X56139	Glycine max lipoxygenase. sc514.

AAA96817.1	U26457	Glycine max lipoxygenase. vlxC.
AAG42354.1	AF234983	Phaseolus vulgaris lipoxygenase.
AAG18376.1	AF283894	Zantedeschia aethiopica lipoxygenase. lox2.
AAD39093.1	AF095895	Oryza sativa catalyzes the addition of molecular oxygen to fatty acid. lipoxygenase. CM-LOX1.
CAC04380.1	AJ293015	Pisum sativum lipoxygenase. lox1:Ps:7.
CAA45088.1	X63525	Phaseolus vulgaris lipoxygenase. loxA.
AAB18970.2	U76687	Phaseolus vulgaris lipoxygenase. PvLOX2.
AAC49159.1	U36191	Glycine max linoleate:oxygen oxidoreductase. lipoxygenase. lox7.
AAA03726.1	U04785	Glycine max lipoxygenase.
CAA45086.1	X63521	Phaseolus vulgaris lipoxygenase.
SEQ ID NO: 741		
AAG28436.1	AF195029	Glycine max plasma membrane Ca2+-ATPase. SCA2.
AAG28435.1	AF195028	Glycine max plasma membrane Ca2+-ATPase. SCA1.
CAA68234.1	X99972	Brassica oleracea calmodulin-stimulated calcium-ATPase.
AAD31896.1	AF145478	Mesembryanthemum crystallinum calcium ATPase.
BAA90510.2	AP001111	Oryza sativa rice EST AU030811, similar to rice Ca2+-ATPase (U82966).
AAD11618.1	AF050496	Lycopersicon esculentum Ca2+-ATPase. LCA1B; alternative transcript.
AAD11617.1	AF050495	Lycopersicon esculentum Ca2+-ATPase. LCA1A; alternative transcript.
AAA34138.1	M96324	Lycopersicon esculentum The calcium ATPase is a calcium ion pump. Ca2+-ATPase. LCA1.
CAA63790.1	X93592	Dunaliella bioculata P-type ATPase. ca1. calcium pumping; CA1.
AAF73985.1	AF096871	Zea mays calcium pump. calcium ATPase. cap1.

AAB58910.1	U82966	Oryza sativa Ca2+-ATPase.
AAD46188.1	AF156691	Nicotiana plumbaginifolia plasma membrane proton ATPase. pma9.
AAB17186.1	U72148	Lycopersicon esculentum plasma membrane H+-ATPase. LHA4. plasma membrane proton pumping ATPase.
CAA47275.1	X66737	Nicotiana plumbaginifolia plasma membrane H+-ATPase. pma4.
CAA54045.1	X76535	Solanum tuberosum H(+) -transporting ATPase. PHA2.
AAD46186.1	AF156679	Nicotiana plumbaginifolia plasma membrane proton ATPase. pma6.
CAA59800.1	X85805	Zea mays H(+) -transporting ATPase. MHA-2.
BAA06629.1	D31843	Oryza sativa plasma membrane H+-ATPase. OSA2.
AAB35314.2	S79323	Vicia faba plasma membrane H(+) -ATPase precursor. plasma membrane H(+) -ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.
CAA59799.1	X85804	Phaseolus vulgaris H(+) -transporting ATPase. BHA-1.
AAB41898.1	U84891	Mesembryanthemum crystallinum plasma membrane proton pump. H+ -transporting ATPase. PMA.
AAA34094.1	M80489	Nicotiana plumbaginifolia plasma membrane H+ ATPase. pma1.
AAB84202.2	AF029256	Kosteletzky virginica plasma membrane proton ATPase. ATP1.
AAA34052.1	M27888	Nicotiana plumbaginifolia H+ -translocating ATPase.
AAA34173.1	M60166	Lycopersicon esculentum H+ -ATPase. LHA1.
AAA34098.1	M80490	Nicotiana plumbaginifolia plasma membrane H+ ATPase. pma3.
AAF98344.1	AF275745	Lycopersicon esculentum plasma membrane H+-ATPase. LHA2. P-type ion pump.
AAD55399.1	AF179442	Lycopersicon esculentum plasma membrane H+-ATPase isoform LHA2. LHA2.
CAC29436.1	AJ310524	Vicia faba P-type H+-ATPase. ha5. predominantly expressed in guard cells and flowers.
BAA08134.1	D45189	Zostera marina plasma membrane H+-ATPase. zha1.

BAA01058.1	D10207	Oryza sativa H-ATPase. OSA1.
CAB69824.1	AJ271439	Prunus persica plasma membrane H ⁺ ATPase. PPA1.
CAA54046.1	X76536	Solanum tuberosum H(+) -transporting ATPase. PHA1.
AAB60276.1	U09989	Zea mays H(+) -transporting ATPase. Mha1.
CAB69823.1	AJ271438	Prunus persica plasma membrane H ⁺ ATPase. PPA2.
AAK31799.1	AY029190	Lilium longiflorum plasma membrane H ⁺ ATPase. LILHA1.
BAA37150.1	AB022442	Vicia faba p-type H ⁺ -ATPase. VHA2.
CAC29435.1	AJ310523	Vicia faba P-type H ⁺ -ATPase. vha4. predominantly expressed in flowers.
CAB85495.1	AJ132892	Medicago truncatula proton pump. H ⁺ -ATPase. ha1.
CAB85494.1	AJ132891	Medicago truncatula proton pump. H ⁺ -ATPase. ha1.
AAD46187.1	AF156683	Nicotiana plumbaginifolia plasma membrane proton ATPase. pma8.
AAD29712.1	AF140499	Oryza sativa chloroplast envelope calcium ATPase precursor.
AAK32118.1	AF308816	Hordeum vulgare plasmalemma H ⁺ -ATPase 1.
AAG01028.1	AF289025	Cucumis sativus plasma membrane H ⁺ -ATPase.
AAF97591.1	AF263917	Lycopersicon esculentum plasma membrane proton ATPase. LHA8.
AAA81348.1	U38965	Vicia faba p-type H ⁺ -ATPase. VHA2.
AAA20600.1	U08984	Zea mays plasma-membrane H ⁺ ATPase. Zmpma1.
AAA20601.1	U08985	Zea mays plasma-membrane H ⁺ ATPase. Zmpma1.
AAK32119.1	AF308817	Hordeum vulgare plasmalemma H ⁺ -ATPase 2.
SEQ ID NO: 742		
AAD02548.1	AF049922	Petunia x hybrida PGPS/D6. PGPS/D6. ER lumen protein retaining receptor homolog; putative HDEL receptor.
SEQ ID NO: 744		

AAG13424.1 AC051634 Oryza sativa
putative mitochondrial inner membrane protein. OSJNBb0018B10.5.

AAG46068.1 AC079830 Oryza sativa
putative inner mitochondrial membrane protein. OSJNBb0009F04.14.

SEQ ID NO: 746

BAA32557.1 AB017159 Daucus carota
citrate synthase. DcCS.

AAA82743.1 U19481 Citrus maxima
synthesis of citrate from oxaloacetate and acetylCoA. citrate synthase precursor. cit.

AAG28777.1 AF302906 Oryza sativa
citrate synthase. similar to putative Oryza sativa citrate synthase in GenBank Accession Number AC004521.

CAA59008.1 X84226 Nicotiana tabacum
citrate synthase. cit1.

CAA52976.1 X75082 Solanum tuberosum
mitochondrial citrate-synthase. ethanolamine ammonia-lyase.

BAA82390.1 AP000367 Oryza sativa
ESTs C96653(C10531),C96654(C10531),C28571(C61641) correspond to a region of the predicted gene.; Similar to citrate synthetase. (AC004521).

CAA59010.1 X84228 Beta vulgaris
citrate (si)-synthase. cit1.

CAA59009.1 X84227 Populus x generosa
citrate (si)-synthase. cit1.

BAA07328.1 D38132 Cucurbita sp.
conversion of oxaloacetate to citrate in the glyoxylate cycle. glyoxysomal citrate synthase.

SEQ ID NO: 750

AAA85365.1 L42466 Picea glauca
ethylene-forming enzyme. EFE.

AAC95363.1 AF104925 Solanum chacoense
2-oxoglutarate-dependent dioxygenase. SPP2. pollination and fertilization induced gene.

BAA75309.1 AB023790 Ipomoea batatas
flavanone 3-hydroxylase. f3h III.

BAA75308.1 AB023789 Ipomoea batatas
flavanone 3-hydroxylase. f3h II.

BAA75306.1 AB023787 Ipomoea batatas
anthocyanidin synthase. ans II.

AAC48922.1 U06047 Vigna radiata
1-aminocyclopropane-1-carboxylate oxidase homolog.

SEQ ID NO: 751

BAB40010.1 AP003021 Oryza sativa
putative wall-associated kinase 2. P0503E05.12.

BAA95893.1 AP002071 Oryza sativa
Similar to Arabidopsis thaliana wak4 gene; wall-associated kinase 4. (AJ009695).

BAB40015.1	AP003021	Oryza sativa putative wall-associated kinase 1. P0503E05.18.
BAA92221.1	AP001278	Oryza sativa Similar to <i>Arabidopsis thaliana</i> chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	Oryza sativa Similar to putative Ser/Thr protein kinase. (AC004218).
BAB40021.1	AP003021	Oryza sativa putative wall-associated kinase 2. P0503E05.25. contains EST C24950(S16264).
CAB51834.1	00069	Oryza sativa 11332.5. contains eukaryotic protein kinase domain PF.
AAB09771.1	U67422	Zea mays CRINKLY4 precursor. cr4. receptor kinase homolog.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK11566.1	AF318490	Lycopersicon hirsutum Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAB40022.1	AP003021	Oryza sativa putative wall-associated kinase 1. P0503E05.26.
CAA97692.1	Z73295	Catharanthus roseus receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1A <i>Arabidopsis thaliana</i> . P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAK11674.1	AF339747	Lophopyrum elongatum protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
BAA90808.1	AP001168	Oryza sativa Similar to putative receptor-like protein kinase (AL035679).
AAF76313.1	AF220603	Lycopersicon esculentum Pto kinase. LescPth5.
AAB47421.1	U59316	Lycopersicon esculentum serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.

AAB47423.1 U59315 *Lycopersicon pimpinellifolium*
serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease
resistance gene.

AAC48914.1 U02271 *Lycopersicon pimpinellifolium*
protein kinase.

AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*
Pto kinase.

AAG59657.1 AC084319 *Oryza sativa*
putative protein kinase. OSJNBa0004B24.20.

AAK11567.1 AF318491 *Lycopersicon hirsutum*
Pto-like protein kinase F. LhirPtoF.

AAK21965.1 AY028699 *Brassica napus*
receptor protein kinase PERK1.

AAG25966.1 AF302082 *Nicotiana tabacum*
cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly
after cytokinin treatment.

AAK11569.1 AF318493 *Lycopersicon hirsutum*
Pto-like protein kinase D. LhirPtoD.

AAF66615.1 AF142596 *Nicotiana tabacum*
LRR receptor-like protein kinase.

AAG03090.1 AC073405 *Oryza sativa*
Similar to an *Arabidopsis* somatic embryogenesis receptor-like kinase (AC007504).

BAA87853.1 AP000816 *Oryza sativa*
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative
NAK-like Ser/Thr protein kinase. (AF001308).

BAA83373.1 AP000391 *Oryza sativa*
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar
to receptor protein kinase, ERECTA (AC004484).

BAA84787.1 AP000559 *Oryza sativa*
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar
to receptor protein kinase, ERECTA (AC004484).

CAA74662.1 Y14286 *Brassica oleracea*
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular
kinase domain: from 1413.

CAA67145.1 X98520 *Brassica oleracea*
receptor-like kinase. SFR2.

CAA73133.1 Y12530 *Brassica oleracea*
serine /threonine kinase. ARLK.

AAK11568.1 AF318492 *Lycopersicon hirsutum*
Pto-like protein kinase B. LhirPtoB.

BAA78764.1 AB023482 *Oryza sativa*
ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar
to *Arabidopsis thaliana* APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).

AAK00425.1 AC069324 Oryza sativa
Putative protein kinase. OSJNBa0071K19.11.

AAK31267.1 AC079890 Oryza sativa
putative protein kinase. OSJNBb0089A17.2.

BAA94509.1 AB041503 Populus nigra
protein kinase 1. PnPK1.

BAA94510.1 AB041504 Populus nigra
protein kinase 2. PnPK2.

SEQ ID NO: 752

BAB39155.1 AB048713 Pisum sativum
SCARECROW. PsSCR.

AAG13663.1 AF263457 Zea mays
transcription factor. SCARECROW. SCR. ZmSCR.

BAA90816.1 AP001168 Oryza sativa
Similar to SCARECROW (U62798).

AAC98090.1 AF067400 Zea mays
Scl1 protein. Scl1. Scarecrow-like; similar to Zea mays sequence presented in GenBank Accession Number T18310.

BAB39156.1 AB048714 Pisum sativum
SCARECROW. PsSCR.

SEQ ID NO: 753

AAF21901.1 AF109392 Brassica napus
ligand gated channel-like protein. glutamate receptor homolog.

SEQ ID NO: 757

CAA92821.1 Z68504 Oryza sativa
3-hydroxy-3-methylglutaryl-CoA reductase.

AAA33360.1 M74800 Hevea brasiliensis
3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.

CAA70440.1 Y09238 Zea mays
3-hydroxy-3-methylglutaryl coenzyme A reductase.

AAB69727.1 U72146 Camptotheca acuminata
3-hydroxy-3-methylglutaryl coenzyme A reductase. converts HMGC-CoA in mevalonate precursor for isoprenoid compounds; HMGR; hmg2; similar to protein encoded by GenBank Accession Number L10390.

AAD08820.1 U43961 Oryza sativa
3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.

AAA68965.1 U14624 Artemisia annua
3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM1.

AAD47596.1 AF142473 Artemisia annua
HMG-CoA reductase. HMGR1.

AAD03789.1 U43711 Morus alba
catalyzes the final step in mevalonate pathway. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR.

AAA33108.1	M96068	<i>Catharanthus roseus</i>
		hydroxymethylglutaryl-CoA reductase. HMGR.
CAA48610.1	X68651	<i>Raphanus sativus</i>
		hydroxymethylglutaryl-CoA reductase (NADPH). HMG1.
AAA93498.1	L01400	<i>Solanum tuberosum</i>
		convert HMG-CoA into mevalonate. hydroxymethylglutaryl coenzyme A reductase. hmgr. putative.
AAA68966.1	U14625	<i>Artemisia annua</i>
		3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM4.
AAB52552.1	U51986	<i>Solanum tuberosum</i>
		HMG-CoA reductase.
CAA48611.1	X68652	<i>Raphanus sativus</i>
		hydroxymethylglutaryl-CoA reductase (NADPH). HMG2.
BAA93631.1	AB022690	<i>Solanum tuberosum</i>
		3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG3.
AAB62581.1	U68072	<i>Lycopersicon esculentum</i>
		3-hydroxy-3-methylglutaryl CoA reductase 2. HMG2.
AAA34169.1	M63642	<i>Lycopersicon esculentum</i>
		3-hydroxy-3-methylglutaryl coenzyme A reductase. hmg2.
AAB69726.1	U72145	<i>Camptotheca acuminata</i>
		converts HMGCoA to mevalonate. 3-hydroxy-3-methylglutaryl coenzyme a reductase. hmg3. HMGR.
AAB52551.1	U51985	<i>Solanum tuberosum</i>
		HMG-CoA reductase.
AAA33040.1	L10390	<i>Camptotheca acuminata</i>
		3-hydroxy-3-methylglutaryl coA reductase.
AAD28179.1	AF110383	<i>Capsicum annum</i>
		3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR2M. HMGR.
BAB20771.1	AB041031	<i>Solanum tuberosum</i>
		3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG2.
AAB53748.1	U95816	<i>Oryza sativa</i>
		3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.
AAC05088.1	AF038045	<i>Gossypium hirsutum</i>
		catalyzes the synthesis of mevalonate from hmg-coA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1. hmg1. hmg-coA reductase 1; HMGR1.
CAA45181.1	X63649	<i>Nicotiana sylvestris</i>
		catalyses synthesis of mevalonate. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR. endoplasmic reticulum location.
CAA38469.1	X54659	<i>Hevea brasiliensis</i>
		hydroxymethylglutaryl-CoA reductase. HMGR1.
CAA38467.1	X54657	<i>Hevea brasiliensis</i>
		hydroxymethylglutaryl-CoA reductase. HMGR1.

AAD38873.1	AF110382	Oryza sativa 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR3G. HMG-CoA reductase.
BAA36291.1	AB021862	Cucumis melo HMG-CoA reductase. Cm-HMGR. putative.
AAB87727.1	U60452	Nicotiana tabacum hydroxy-methylglutaryl-coenzyme A reductase. HMGR1.
AAC05089.1	AF038046	Gossypium hirsutum catalyzes the synthesis of mevalonate from hmg-coA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2. hmg2. hmg-coA reductase 2; HMGR2.
AAC15475.1	AF034760	Tagetes erecta 3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAC15476.1	AF034761	Tagetes erecta 3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAA21720.1	L28995	Oryza sativa conversion of hydroxymethylglutaryl coenzyme A to mevalonate. 3-hydroxy-3-methylglutaryl coenzyme A reductase. putative.
AAA33358.1	M74798	Hevea brasiliensis 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
AAC72378.1	AF096838	Solanum tuberosum 3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAB04043.1	L40938	Lycopersicon esculentum HMGR CoA reductase. HMGR1.
CAA38468.1	X54658	Hevea brasiliensis hydroxymethylglutaryl-CoA reductase. HMGR2.
CAA52787.1	X74783	Lithospermum erythrorhizon 3-hydroxy-3-methyl glutaryl coenzyme A reductase. Lehmgr1.
AAD09278.1	U97683	Glycine max catalyzes the synthesis of mevalonate, the specific precursor of all isoprenoid compounds present in plants. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMG-CoA reductase.
AAG43469.1	AF196964	Bixa orellana catalyzes mevalonate synthesis from hmg-CoA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase.
BAA09705.1	D63389	Cucumis sativus 3-hydroxy-3-methylglutaryl CoA reductase.
AAB47161.1	S82272	Gossypium barbadense 3-hydroxy-3-methylglutaryl coenzyme A reductase. /gene="3-hydroxy-3-methylglutaryl coenzyme A reductase,. This sequence comes from Fig. 2; 3-hydroxy-3-methylglutaryl CoA reductase; HMGR.
AAA33359.1	M74799	Hevea brasiliensis 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
AAC37434.1	L34827	Solanum tuberosum HMG-CoA reductase. hmgl gene family.

AAC37432.1	L34825	Solanum tuberosum HMG-CoA reductase. hmg1 gene family.
AAC37435.1	L34828	Solanum tuberosum HMG-CoA reductase. hmg1 gene family.
AAC37433.1	L34826	Solanum tuberosum HMG-CoA reductase. hmg1 gene family.
AAC37431.1	L34823	Solanum tuberosum HMG-CoA reductase. hmg1 gene family.
		SEQ ID NO: 761
CAA96512.1	Z71980	Malus x domestica knotted1-like homeobox protein.
BAA25921.1	AB004797	Nicotiana tabacum NTH23. homeobox gene.
AAD09582.1	U76409	Lycopersicon esculentum homeobox 1 protein. THox1. homeodomain protein.
AAC49918.1	AF000142	Lycopersicon esculentum class II knotted-like homeodomain protein. LeT12.
BAA08552.1	D49704	Oryza sativa OSH45. OSH44 transcript homeobox gene.
BAB18585.1	AB043957	Ceratopteris richardii CRKNOX3. crknox3. knotted1-like homeodomain protein.
AAD00253.1	U76410	Lycopersicon esculentum homeobox 2 protein. THox2. homeodomain protein.
CAA82314.1	Z29073	Brassica napus homeodomain-containing protein. Bnhd1.
BAA77822.1	AB007628	Oryza sativa HOS59. homeobox gene.
BAA77823.1	AB007629	Oryza sativa HOS66. homeobox gene.
AAB81079.1	AF022390	Hordeum vulgare knotted class 1 homeodomain protein. k. similar to the hooded gene product encoded by GenBank Accession Number X83518; similar to the maize knotted-1 gene product encoded by GenBank Accession Number X61308.
AAF32399.1	AF224499	Triticum aestivum KNOTTED-1-like homeobox protein b. knox1b. KNOX1b.
BAA76750.1	AB025573	Nicotiana tabacum KN1-type homeobox protein. NTH1.
AAF32400.1	AF224500	Triticum aestivum KNOTTED-1-like homeobox protein d. knox1d. KNOX1d.
AAC49917.1	AF000141	Lycopersicon esculentum class I knotted-like homeodomain protein. LeT6.
BAA25546.1	AB004785	Nicotiana tabacum NTH15. homeobox gene.

AAF32398.1 AF224498 *Triticum aestivum*
KNOTTED-1-like homeobox protein a. knox1a. KNOX1.

AAD13611.1 AF100455 *Zea mays*
knotted class 1 homeodomain protein liguleless3. lg3.

AAC84001.1 AF063248 *Picea abies*
homeobox protein.

AAC33008.1 AF080104 *Pisum sativum*
knotted1-like class I homeodomain protein. PsKn1.

AAD00692.1 U90092 *Picea mariana*
homeobox transcription factor SKN2. knotted1-like homeobox gene.

AAC32262.1 AF063307 *Pisum sativum*
Knox class 1 protein. Hop1.

BAA03959.1 D16507 *Oryza sativa*
homeobox protein. OSH1.

AAG27464.1 AF308454 *Medicago truncatula*
knotted class I homeodomain KNOX.

AAD00691.1 U90091 *Picea mariana*
homeobox transcription factor SKN1. knotted1-like homeobox gene.

AAC32817.1 AF050180 *Oryza sativa*
transcription factor. KNOX class homeodomain protein. OsKn2.

BAA79226.1 AB028885 *Oryza sativa*
knotted1-type homeobox protein OSH71. OSH71.

BAA79224.1 AB028883 *Oryza sativa*
knotted1-type homeobox protein OSH6. OSH6.

BAA77818.1 AB007624 *Oryza sativa*
HOS9. homeobox gene.

BAB19772.1 AP002881 *Oryza sativa*
putative knotted1-type homeobox protein. P0035H10.13.

AAF23753.2 AF193813 *Brassica oleracea*
shoot meristemless. Stm. homeodomain protein.

AAD00251.1 U76407 *Lycopersicon esculentum*
knotted 2 protein. TKn2. homeodomain protein.

CAA96510.1 Z71978 *Malus x domestica*
kn1-like protein.

BAA31688.1 AB016071 *Oryza sativa*
OSH15. homeobox gene.

BAA77817.1 AB007623 *Oryza sativa*
HOS3. homeobox gene.

BAB18582.1 AB043954 *Ceratopteris richardii*
CRKNOX1. crknox1. knotted1-like homeodomain protein.

BAA76903.1 AB025713 *Nicotiana tabacum*
homeobox 9. NTH9.

AAD00252.1 U76408 *Lycopersicon esculentum*
knotted 3 protein. TKn3. homeodomain protein.

BAB18584.1 AB043956 *Ceratopteris richardii*
CRKNOX2. crknox2. knotted1-like homeodomain protein.

CAA96511.1 Z71979 *Malus x domestica*
kn1-like protein.

AAA20882.1 L13663 *Glycine max*
SBH1. Sbh1. soybean homeobox-containing gene.

CAB88029.1 AJ276389 *Dendrobium grex Madame Thong-In*
transcription factor. knotted1-like homeobox protein.

SEQ ID NO: 762

AAB65776.1 U97521 *Vitis vinifera*
class IV endochitinase. VvChi4A.

AAB65777.1 U97522 *Vitis vinifera*
class IV endochitinase. VvChi4B.

CAA53626.1 X76041 *Triticum aestivum*
endochitinase. CHI.

AAG53609.1 AF280437 *Secale cereale*
31.7 kDa class I endochitinase-antifreeze protein precursor. cht9.

BAA03750.1 D16222 *Oryza sativa*
endochitinase. Cht-2.

AAA32986.1 M95835 *Brassica napus*
endochitinase. Ch25.

BAA03749.1 D16221 *Oryza sativa*
endochitinase. Cht-1.

AAB01895.1 U48687 *Castanea sativa*
endochitinase.

SEQ ID NO: 763

AAA34065.1 M94135 *Nicotiana tabacum*
chloroplast carbonic anhydrase.

AAA34057.1 L19255 *Nicotiana tabacum*
carbonic anhydrase.

AAB65822.1 U55838 *Populus tremula x Populus tremuloides*
carbonic anhydrase. CA1b. EC 4.2.1.1.

AAC49785.1 U55837 *Populus tremula x Populus tremuloides*
carbonic anhydrase. CA1a. EC 4.2.1.1.

AAA34026.1 M27295 *Spinacia oleracea*
carbonic anhydrase precursor.

AAA34027.1 J05403 *Spinacia oleracea*
carbonic anhydrase (EC 4.2.1.1).

AAA86993.1 U19738 *Flaveria linearis*
reversible hydration of carbon dioxide. carbonic anhydrase 1.

AAA86942.1	U08402	Flaveria brownii carbonic anhydrase.
AAA86992.1	U19737	Flaveria pringlei reversible hydration of carbon dioxide. carbonic anhydrase.
AAA86939.1	U08398	Flaveria bidentis carbonic anhydrase.
AAD27876.2	AF139464	Vigna radiata carbonic anhydrase. CipCa1.
AAA33652.1	M63627	Pisum sativum carbonic anhydrase.
AAD29050.1	AF132855	Gossypium hirsutum interconversion of CO2 and HCO3-. carbonic anhydrase isoform 2. CA2. zinc metalloenzyme; carbonate dehydratase.
AAD29049.1	AF132854	Gossypium hirsutum interconversion of CO2 and HCO3-. carbonic anhydrase isoform 1. CA1. zinc metalloenzyme; carbonate dehydratase.
AAA86994.1	U19740	Flaveria linearis reversible hydration of carbon dioxide. carbonic anhydrase 2.
CAB43571.1	AJ239132	Glycine max hydration of carbon dioxide. carbonic anhydrase. ca1.
CAA63712.1	X93312	Medicago sativa Carbonic anhydrase. ca1.
AAA86945.1	U08403	Zea mays carbonic anhydrase.
AAA86944.1	U08401	Zea mays carbonic anhydrase.
AAC41656.1	L36959	Hordeum vulgare carbonic anhydrase. putative.
AAA86943.1	U08404	Oryza sativa carbonic anhydrase. nuclear encoded, localized to chloroplast.
AAD56038.1	AF182806	Oryza sativa carbonic anhydrase 3. ca3.
BAA31953.1	AB016283	Oryza sativa carbonic anhydrase.
AAA69027.1	U19739	Urochloa panicoides reversible hydration of carbon dioxide. carbonic anhydrase 2.
AAA69028.1	U19741	Urochloa panicoides reversible hydration of carbon dioxide. carbonic anhydrase 1.
BAA95793.1	AB009887	Nicotiana tabacum carbonic anhydrase. carbonic anhydrase.
AAF78507.1	AF195204	Pyrus pyrifolia carbonic anhydrase isoform 1. CA1.

AAC33484.1 U49976 Cocomyx sp. PA
beta-type carbonic anhydrase beta-CA1.

AAA18560.1 M95073 Zea mays
putative. silimar to carbonic anhydrases.

AAB19184.1 U41190 Chlamydomonas reinhardtii
carbonic anhydrase precursor. beta-CA2.

AAB19183.1 U41189 Chlamydomonas reinhardtii
carbonic anhydrase precursor. beta-CA1.

AAC49887.1 U80804 Chlamydomonas reinhardtii
beta-carbonic anhydrase. ca1. beta-CA1.

AAC49888.1 U80805 Chlamydomonas reinhardtii
beta-carbonic anhydrase. ca2. beta-CA2.

SEQ ID NO: 764

AAC06027.1 AF052058 Vigna unguiculata
iron storage and mobilization in plants. ferritin subunit cowpea2 precursor.

AAD50644.1 AF133814 Solanum tuberosum
ferritin 1. F1.

AAB53099.1 U68217 Brassica napus
iron binding protein. ferritin. LSC30.

AAA33959.1 M64337 Glycine max
ferritin light chain. ferritin.

AAA34016.1 M72894 Glycine max
ferritin light chain. SOF-H2.

CAA58146.1 X83076 Zea mays
ferritin. Fer1.

AAB18928.1 U31648 Glycine max
iron storage protein. ferritin.

CAA65771.1 X97059 Medicago sativa
iron storage. ferritin. FER. abscissic acid regulated.

CAA43663.1 X61391 Zea mays
ferritin.

CAA58147.1 X83077 Zea mays
ferritin. Fer2.

AAC06026.1 AF052057 Vigna unguiculata
iron storage and mobilization in plants. ferritin subunit cowpea3 precursor.

CAA43664.1 X61392 Zea mays
ferritin.

CAA51786.1 X73369 Pisum sativum
ferritin.

CAA45763.1 X64417 Pisum sativum
ferritin-precursor.

CAA41213.1	X58274	Phaseolus vulgaris ferritin. pfe.
AAA33958.1	M58336	Glycine max ferritin light chain. SOF-5L.
CAB42587.1	AJ238628	Chlorella protothecoides putative ferritin. dee188.
BAB17852.1	AB042612	Nicotiana tabacum ferritin 1. tob-fer-1. putative.
AAC15241.1	AF028072	Pinus taeda ferritin.
CAA47983.1	X67755	Vigna unguiculata ferritin 2. pfe2.
CAA47982.1	X67754	Vigna unguiculata ferritin 1. pfe1.
CAA47984.1	X67756	Vigna unguiculata ferritin 5. pfe5.
AAC12282.1	AF052511	Glycine max iron storage and mobilization. ferritin 2. soybean 2; cowpea 2 homolog.
AAC12281.1	AF052513	Glycine max iron storage and mobilization. ferritin 1. soybean 1; cowpea 1 homolog.
SEQ ID NO: 765		
AAC36697.1	AF075579	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAC10358.1	AJ277086	Nicotiana tabacum protein phosphatase 2C. PP2C1.
CAB90633.1	AJ277743	Fagus sylvatica protein phosphatase 2C (PP2C). pp2C1. ABA-induced protein.
AAD17804.1	AF092431	Lotus japonicus nodule-enhanced protein phosphatase type 2C. NPP2C1.
CAC10359.1	AJ277087	Nicotiana tabacum protein phosphatase 2C. PP2C2.
CAC09575.1	AJ298987	Fagus sylvatica protein phosphatase 2C (PP2C). pp2Cf1.
CAA72341.1	Y11607	Medicago sativa protein phosphatase 2C. MP2C.
CAB61839.1	AJ242803	Sporobolus stapfianus putative serine/threonine phosphatase type 2c.
AAD17805.1	AF092432	Lotus japonicus protein phosphatase type 2C. PP2C2.
AAG43835.1	AF213455	Zea mays protein phosphatase type-2C. pp2c-1. PP2C-1.

AAG46118.1	AC073166	Oryza sativa putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.
AAG13599.1	AC051633	Oryza sativa putative protein phosphatase-2C. OSJNBb0015I11.26.
AAC36698.1	AF075580	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
BAB12036.1	AP002820	Oryza sativa putative protein phosphatase. P0702D12.18.
AAC36700.1	AF075582	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
AAC36699.1	AF075581	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
AAK20060.1	AC025783	Oryza sativa putative protein phosphatase 2C. OSJNBa0001O14.1.
AAD11430.1	AF097667	Mesembryanthemum crystallinum protein phosphatase 2C homolog. PP2C.
CAB90634.1	AJ277744	Fagus sylvatica protein phosphatase 2C (PP2C). pp2C2. ABA and calcium induced protein.
AAC35951.1	AF079355	Mesembryanthemum crystallinum protein phosphatase-2c. PP2C.
AAF19804.1	AF180355	Brassica oleracea ABI1 protein. ABI1. similar to Arabidopsis thaliana ABI1.
AAB93832.1	U81960	Zea mays kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases; type 2C protein phosphatase. kinase associated protein phosphatase. KAPP.
AAC26828.1	AF075603	Oryza sativa kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases. kinase associated protein phosphatase. kapp. type 2C protein phosphatase.
CAC09576.1	AJ298988	Fagus sylvatica protein phosphatase 2C (PP2C). pp2Cf2.
SEQ ID NO: 766		
AAG08959.1	AF122051	Solanum tuberosum tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08960.1	AF122052	Solanum tuberosum tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08961.1	AF122053	Solanum tuberosum tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.

BAA88169.1	AP000836	Oryza sativa Similar to putative transcription factor (AF062890).
BAA88205.1	AP000837	Oryza sativa Similar to putative transcription factor (AF062890).
AAF34434.1	AF172282	Oryza sativa myb-like protein. DUPR11.29.
AAF78890.1	AF189788	Hordeum vulgare putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.
AAF78889.1	AF189787	Hordeum vulgare putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.
AAF67053.1	AF190304	Adiantum raddianum c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF67052.1	AF190303	Adiantum raddianum c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF78888.1	AF189786	Physcomitrella patens putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.
AAF78887.1	AF189785	Physcomitrella patens putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.
AAF43043.1	AF236059	Papaver rhoeas putative Myb-related domain. pmr.
BAA94769.1	AP001859	Oryza sativa Similar to Arabidopsis thaliana chromosome 4, BAC clone F4D11; putative myb-protein. (AL022537).
AAF67050.1	AF190301	Secale cereale c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF67051.1	AF190302	Secale cereale c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
CAA78388.1	Z13998	Petunia x hybrida DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.
BAB39987.1	AP003020	Oryza sativa putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
BAB39972.1	AP003018	Oryza sativa putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).
CAA72218.1	Y11415	Oryza sativa myb.
BAA81731.1	AB029160	Glycine max GmMYB29A1.
BAA81730.1	AB029159	Glycine max GmMYB29A1.

CAA72217.1	Y11414	Oryza sativa myb.
BAA81736.1	AB029165	Glycine max GmMYB29B2.
BAB12688.1	AP002746	Oryza sativa putative MYB family transcription factor. P0671B11.3. contains ESTs AU082307(E0784),C72014(E0784).
BAA99440.1	AP002743	Oryza sativa putative MYB family transcription factor. P0710E05.27. contains ESTs AU082307(E0784),C72014(E0784).
AAB41101.1	U72762	Nicotiana tabacum transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.
BAA88223.1	AB028651	Nicotiana tabacum myb-related transcription factor LBM3. lbm3.
BAA23340.1	D88620	Oryza sativa transfactor. OSMYB4. Osmyb4.
BAA93038.1	AP001552	Oryza sativa EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to <i>Arabidopsis thaliana</i> putative transcription factor (AF062916).
AAA33067.1	L04497	Gossypium hirsutum MYB A; putative.
BAA81733.2	AB029162	Glycine max GmMYB29A2.
BAA88222.1	AB028650	Nicotiana tabacum myb-related transcription factor LBM2. lbm2.
CAB43399.1	AJ006292	Antirrhinum majus Myb-related transcription factor mixta-like 1. mybml1.
BAA81732.1	AB029161	Glycine max GmMYB29A2.
AAG28525.1	AF198498	Nicotiana tabacum anther-specific myb-related protein 2. mybAS2. NtMYBAS2; contains tandem R2, R3 myb domains similar to c-myb family.
CAA50226.1	X70881	Hordeum vulgare MybHv33. myb3.
CAA50223.1	X70878	Hordeum vulgare MybHv33. myb3.
CAA78387.1	Z13997	Petunia x hybrida DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
CAA67000.1	X98355	Oryza sativa activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.

AAC19616.1	AF336283	Gossypium hirsutum GHMYB25. similar to myb; contains an unspliced intron.
AAG28526.1	AF198499	Nicotiana tabacum anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
CAA78386.1	Z13996	Petunia x hybrida DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
CAA66952.1	X98308	Lycopersicon esculentum THM18. myb-related transcription factor.
BAA23341.1	D88621	Oryza sativa transfactor. OSMYB5. Osmyb5.
CAA50221.1	X70876	Hordeum vulgare MybHv5. myb2.
AAC19611.1	AF336278	Gossypium hirsutum BNLGH1233. bnlghi6233. similar to myb.
AAC04716.1	AF034130	Gossypium hirsutum putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-D. similar to MYB A encoded by GenBank Accession Number L04497.
CAA61021.1	X87690	Hordeum vulgare transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.
AAG22863.1	AY008692	Hordeum vulgare transcription factor GAMyb. Gamyb.
SEQ ID NO: 767		
CAB08111.1	Z94180	Lycopersicon esculentum branched chain alpha-keto acid dehydrogenase E1-alpha subunit.
CAA81558.1	Z26949	Solanum tuberosum subunit of the mitochondrial pyruvate dehydrogenase complex. E1 alpha subunit of pyruvate dehydrogenase precursor.
AAC72195.1	AF069911	Zea mays pyruvate dehydrogenase E1 alpha subunit.
AAG43499.1	AF209924	Lycopersicon esculentum pyruvate dehydrogenase.
AAA97411.1	U51918	Pisum sativum pyruvate dehydrogenase E1 alpha subunit.
CAA10992.1	AJ222787	Hordeum vulgare alpha-keto acid dehydrogenase-like protein. homology to branched chain alpha-keto acid dehydrogenase E1-alpha subunit.
SEQ ID NO: 768		
AAF64450.1	AF239928	Euphorbia esula glutathione S-transferase. similar to auxin-inducible GST.

AAG16758.1 AY007560 *Lycopersicon esculentum*
putative glutathione S-transferase T3.

AAG34803.1 AF243368 *Glycine max*
glutathione S-transferase GST 13.

AAG16756.1 AY007558 *Lycopersicon esculentum*
putative glutathione S-transferase T1.

AAG34796.1 AF243361 *Glycine max*
glutathione S-transferase GST 6.

AAG34809.1 AF243374 *Glycine max*
glutathione S-transferase GST 19.

AAG34797.1 AF243362 *Glycine max*
glutathione S-transferase GST 7.

AAG34807.1 AF243372 *Glycine max*
glutathione S-transferase GST 17.

AAG34798.1 AF243363 *Glycine max*
glutathione S-transferase GST 8.

AAG34804.1 AF243369 *Glycine max*
glutathione S-transferase GST 14.

AAG16759.1 AY007561 *Lycopersicon esculentum*
putative glutathione S-transferase T4.

AAG34801.1 AF243366 *Glycine max*
glutathione S-transferase GST 11.

AAG34810.1 AF243375 *Glycine max*
glutathione S-transferase GST 20.

AAG16757.1 AY007559 *Lycopersicon esculentum*
putative glutathione S-transferase T2.

AAC18566.1 AF048978 *Glycine max*
2,4-D inducible glutathione S-transferase, GSTa.

AAG34808.1 AF243373 *Glycine max*
glutathione S-transferase GST 18.

AAG34800.1 AF243365 *Glycine max*
glutathione S-transferase GST 10.

CAA71784.1 Y10820 *Glycine max*
glutathione transferase.

AAG34844.1 AF244701 *Zea mays*
glutathione S-transferase GST 36.

AAG32472.1 AF309379 *Oryza sativa* subsp. *japonica*
putative glutathione S-transferase OsGSTU3.

AAA68430.1 J03679 *Solanum tuberosum*
glutathione S-transferase, gst1, previously called pathogenesis-related protein; prp1-1.

CAA04391.1 AJ000923 *Carica papaya*
glutathione transferase, PGST1.

AAG34831.1 AF244688	Zea mays glutathione S-transferase GST 23.
CAA09187.1 AJ010448	Alopecurus myosuroides glutathione transferase. GST1a.
CAA09188.1 AJ010449	Alopecurus myosuroides glutathione transferase. GST1b.
AAG34802.1 AF243367	Glycine max glutathione S-transferase GST 12.
AAG34805.1 AF243370	Glycine max glutathione S-transferase GST 15.
AAG34832.1 AF244689	Zea mays glutathione S-transferase GST 24.
AAG34837.1 AF244694	Zea mays glutathione S-transferase GST 29.
AAG34836.1 AF244693	Zea mays glutathione S-transferase GST 28.
AAG32471.1 AF309378	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU4.
AAG34849.1 AF244706	Zea mays glutathione S-transferase GST 41.
CAC24549.1 AJ296343	Cichorium intybus x Cichorium endivia glutathione S-transferase. chi-GST1. auxin-induced GST.
AAC32118.1 AF051214	Picea mariana probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAG34795.1 AF243360	Glycine max glutathione S-transferase GST 5.
AAG34841.1 AF244698	Zea mays glutathione S-transferase GST 33.
AAF29773.1 AF159229	Gossypium hirsutum glutathione S-transferase. GST.
SEQ ID NO: 769	
AAG34797.1 AF243362	Glycine max glutathione S-transferase GST 7.
AAG34798.1 AF243363	Glycine max glutathione S-transferase GST 8.
AAG34803.1 AF243368	Glycine max glutathione S-transferase GST 13.
AAG16758.1 AY007560	Lycopersicon esculentum putative glutathione S-transferase T3.
AAF64450.1 AF239928	Euphorbia esula glutathione S-transferase. similar to auxin-inducible GST.

AAG34801.1	AF243366	Glycine max glutathione S-transferase GST 11.
AAG34804.1	AF243369	Glycine max glutathione S-transferase GST 14.
AAG34796.1	AF243361	Glycine max glutathione S-transferase GST 6.
AAG34809.1	AF243374	Glycine max glutathione S-transferase GST 19.
AAG16759.1	AY007561	Lycopersicon esculentum putative glutathione S-transferase T4.
AAG16757.1	AY007559	Lycopersicon esculentum putative glutathione S-transferase T2.
AAG16756.1	AY007558	Lycopersicon esculentum putative glutathione S-transferase T1.
AAG34807.1	AF243372	Glycine max glutathione S-transferase GST 17.
AAG34810.1	AF243375	Glycine max glutathione S-transferase GST 20.
AAG34844.1	AF244701	Zea mays glutathione S-transferase GST 36.
AAG34831.1	AF244688	Zea mays glutathione S-transferase GST 23.
AAC18566.1	AF048978	Glycine max 2,4-D inducible glutathione S-transferase. GSTa.
AAG34832.1	AF244689	Zea mays glutathione S-transferase GST 24.
AAG34808.1	AF243373	Glycine max glutathione S-transferase GST 18.
AAG34837.1	AF244694	Zea mays glutathione S-transferase GST 29.
AAG34800.1	AF243365	Glycine max glutathione S-transferase GST 10.
AAG34836.1	AF244693	Zea mays glutathione S-transferase GST 28.
CAA04391.1	AJ000923	Carica papaya glutathione transferase. PGST1.
CAA71784.1	Y10820	Glycine max glutathione transferase.
AAG34849.1	AF244706	Zea mays glutathione S-transferase GST 41.
AAA68430.1	J03679	Solanum tuberosum glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.

AAG34802.1	AF243367	Glycine max glutathione S-transferase GST 12.
CAC24549.1	AJ296343	Cichorium intybus x Cichorium endivia glutathione S-transferase. chi-GST1. auxin-induced GST.
CAA09187.1	AJ010448	Alopecurus myosuroides glutathione transferase. GST1a.
AAF22518.1	AF118925	Papaver somniferum glutathione S-transferase 2. GST2.
AAG32471.1	AF309378	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU4.
CAA09188.1	AJ010449	Alopecurus myosuroides glutathione transferase. GST1b.
AAF22517.1	AF118924	Papaver somniferum glutathione S-transferase 1. GST1.
AAF22647.1	AF193439	Lycopersicon esculentum glutathione S-transferase/peroxidase. BI-GST/GPX.
AAG32473.1	AF309380	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU2.
AAG32472.1	AF309379	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU3.
SEQ ID NO: 771		
AAG46118.1	AC073166	Oryza sativa putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.
AAG13599.1	AC051633	Oryza sativa putative protein phosphatase-2C. OSJNBb0015I11.26.
BAB12036.1	AP002820	Oryza sativa putative protein phosphatase. P0702D12.18.
AAC36698.1	AF075580	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAA72341.1	Y11607	Medicago sativa protein phosphatase 2C. MP2C.
AAG43835.1	AF213455	Zea mays protein phosphatase type-2C. pp2c-1. PP2C-1.
CAB61839.1	AJ242803	Sporobolus stapfianus putative serine/threonine phosphatase type 2c.
AAD17804.1	AF092431	Lotus japonicus nodule-enhanced protein phosphatase type 2C. NPP2C1.
AAD17805.1	AF092432	Lotus japonicus protein phosphatase type 2C. PP2C2.
AAC36697.1	AF075579	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.

CAB90633.1	AJ277743	Fagus sylvatica protein phosphatase 2C (PP2C). pp2C1. ABA-induced protein.
CAC10358.1	AJ277086	Nicotiana tabacum protein phosphatase 2C. PP2C1.
CAC10359.1	AJ277087	Nicotiana tabacum protein phosphatase 2C. PP2C2.
AAC36700.1	AF075582	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAC09575.1	AJ298987	Fagus sylvatica protein phosphatase 2C (PP2C). pp2Cf1.
AAK20060.1	AC025783	Oryza sativa putative protein phosphatase 2C. OSJNBa0001O14.1.
CAB90634.1	AJ277744	Fagus sylvatica protein phosphatase 2C (PP2C). pp2C2. ABA and calcium induced protein.
AAC35951.1	AF079355	Mesembryanthemum crystallinum protein phosphatase-2c. PP2C.
AAD11430.1	AF097667	Mesembryanthemum crystallinum protein phosphatase 2C homolog. PP2C.
AAB93832.1	U81960	Zea mays kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases; type 2C protein phosphatase. kinase associated protein phosphatase. KAPP.
AAC26828.1	AF075603	Oryza sativa kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases. kinase associated protein phosphatase. kapp. type 2C protein phosphatase.
AAC36699.1	AF075581	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAC09576.1	AJ298988	Fagus sylvatica protein phosphatase 2C (PP2C). pp2Cf2.
SEQ ID NO: 777		
AAD21872.1	AF078082	Phaseolus vulgaris receptor-like protein kinase homolog RK20-1.
AAB93834.1	U82481	Zea mays KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA74661.1	Y14285	Brassica oleracea SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAD52097.1	AF088885	Nicotiana tabacum receptor-like kinase CHRK1. Chrk1.
CAA73134.1	Y12531	Brassica oleracea serine/threonine kinase. BRLK.

CAB41879.1	Y18260	Brassica oleracea SRK15 protein. SRK15. receptor-like kinase.
CAB41878.1	Y18259	Brassica oleracea SRK5 protein. SRK5. receptor-like kinase.
AAA33008.1	M97667	Brassica napus serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus ser /thr kinase. S-locus receptor kinase. srk.
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
AAA33000.1	M76647	Brassica oleracea receptor protein kinase. SKR6.
CAA73133.1	Y12530	Brassica oleracea serine /threonine kinase. ARLK.
AAA62232.1	U00443	Brassica napus S-receptor kinase. protein contains an immunoglobulin-like domain.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
CAA74662.1	Y14286	Brassica oleracea SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAA92837.1	AB032474	Brassica oleracea S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa receptor protein kinase SRK12.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
CAA79355.1	Z18921	Brassica oleracea S-receptor kinase-like protein.
BAB21001.1	AB054061	Brassica rapa S locus receptor kinase. SRK22.
BAA21132.1	D88193	Brassica rapa S-receptor kinase. SRK9 (B.c.).
BAA06285.1	D30049	Brassica rapa S-receptor kinase SRK9.
BAA92836.1	AB032473	Brassica oleracea S18 S-locus receptor kinase. SRK18.
BAA07576.1	D38563	Brassica rapa receptor protein kinase SRK8.
BAB18292.1	AP002860	Oryza sativa putative receptor-like protein kinase. P0409B08.19.
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.

BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
BAB39435.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.2.
BAB07904.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.12.
BAA94518.1	AP001800	Oryza sativa Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
AAG16628.1	AY007545	Brassica napus protein serine/threonine kinase BNK1.
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAF91324.1	AF244890	Glycine max receptor-like protein kinase 3. RLK3. GmRLK3.
BAA82556.1	AB030083	Populus nigra lectin-like protein kinase. PnLPK.
AAF91323.1	AF244889	Glycine max receptor-like protein kinase 2. RLK2. GmRLK2.
AAF91322.1	AF244888	Glycine max receptor-like protein kinase 1. RLK1. GmRLK1.
SEQ ID NO: 779		
AAK31284.1	AC079890	Oryza sativa putative quinone oxidoreductase. OSJNBb0089A17.10.
BAA78050.1	AB027757	Cicer arietinum NADPH oxidoreductase homolog.
BAA83082.1	AB030704	Lithospermum erythrorhizon LEDI-4 protein. LEDI-4. preferentially expressed in darkness; putative NADPH quinone oxidoreductase; similar to zeta-crystallin.
AAG53944.1	AF304461	Triphysaria versicolor quinone-oxidoreductase QR1. TvQR1.
SEQ ID NO: 780		
AAK17067.1	AF254558	Oryza sativa NAC6. NAC6.

BAA89800.1	AB028185	Oryza sativa OsNAC6 protein. OsNAC6.
BAA89799.1	AB028184	Oryza sativa OsNAC5 protein. OsNAC5.
BAA89798.1	AB028183	Oryza sativa OsNAC4 protein. OsNAC4.
BAA89797.1	AB028182	Oryza sativa OsNAC3 protein. OsNAC3.
BAA89801.1	AB028186	Oryza sativa OsNAC7 protein. OsNAC7.
AAF68626.1	AF254124	Medicago truncatula NAC1. NAC1. NAC domain containing protein.
BAA89802.1	AB028187	Oryza sativa OsNAC8 protein. OsNAC8.
BAA78417.1	AB021178	Nicotiana tabacum NAC-domain protein. TERN. elicitor-responsive gene.
SEQ ID NO: 783		
CAA54390.1	X77134	Brassica napus acyl-CoA binding protein.
CAA70200.1	Y08996	Ricinus communis acyl-CoA-binding protein.
CAB56693.1	AJ249833	Digitalis lanata binds medium- and long-chain acyl-coa esters. Acyl-CoA binding protein (ACBP). acbp3.
CAB56694.1	AJ249834	Digitalis lanata binds medium- and long-chain acyl-coa esters. Acyl-CoA binding protein (ACBP). acbp4.
AAB67736.1	U35015	Gossypium hirsutum acyl-CoA-binding protein.
AAB86851.1	AF031541	Fritillaria agrestis acyl-CoA-binding protein. acabp.
SEQ ID NO: 784		
CAA58994.1	X84208	Sinapis alba trypsin inhibitor 2. mti-2.
CAA76116.1	Y16190	Sinapis alba trypsin inhibitor 2. mti-2.
SEQ ID NO: 785		
AAF66242.1	AF243180	Lycopersicon esculentum dicyanin. binuclear blue copper protein; contains two stellacyanins linked together.

AAC32421.1 U65511 *Cucumis sativus*

putative oxygen activation and/or lignin formation. stellacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytocyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Stellacyanins; similar to *Rhus vernicifera* stellacyanin: SwissProt Accession Number P00302; similar to umecyanin: SwissProt Accession Number P42849; similar to mavicyanin; SwissProt Accession Number P80728; similar to BCB encoded by GenBank Accession Number Z15058; similar to F18A8.9, encoded by GenBank Accession Number AC003105; similar to F7F1.27 encoded by GenBank Accession Number AC004669; similar to F9D12.16 encoded by GenBank Accession Number AF077407; glycoprotein.

CAA80963.1 Z25471 *Pisum sativum*
blue copper protein.

AAD10251.1 AF031195 *Triticum aestivum*
blue copper-binding protein homolog. S85.

AAC64163.1 AF093537 *Zea mays*
blue copper protein. similar to pea blue copper protein in GenBank Accession Number Z25471.

CAA10134.1 AJ012693 *Cicer arietinum*
basic blue copper protein.

AAF66243.1 AF243181 *Lycopersicon esculentum*
plantacyanin. naturally occurring cupredoxin with a Val residue in the position of the axial ligand Met; member of the plantacyanin subfamily of a strictly plant-specific family of mononuclear blue copper proteins known as phytocyanins.

CAB65280.1 AJ248323 *Medicago sativa* subsp. x varia
basic blue protein. babl.

AAC32448.1 U76296 *Spinacia oleracea*
plantacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytocyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Plantacyanins; non-glycosylated.

SEQ ID NO: 793

BAA81862.1 AB026295 *Oryza sativa*
Similar to leucoanthocyanidin dioxygenase.(AI440611).

AAB39995.1 U82432 *Dianthus caryophyllus*
anthocyanidin synthase. allele: S; 2-oxoglutarat-dependent dioxygenase.

BAA36554.1 AB011796 *Citrus unshiu*
flavonol synthase. CitFLS.

AAD56580.1 AF184273 *Daucus carota*
leucoanthocyanidin dioxygenase 1. LDOX1. 2-oxoglutarate dependent dioxygenase.

AAD56581.1 AF184274 *Daucus carota*
leucoanthocyanidin dioxygenase 2. LDOX. 2-oxoglutarate dependent dioxygenase.

CAA50498.1 X71360 *Malus* sp.
anthocyanidin hydroxylase. apple equivalent to 'Candi' from *Antirrhinum majus*.

AAD26205.1 AF117269 *Malus x domestica*
anthocyanidin synthase. ANS.

AAB82287.1 AF026058 *Matthiola incana*
anthocyanidin synthase.

CAA80264.1 Z22543 *Petunia x hybrida*
flavonol synthase.

AAF64168.1 AF240764 *Eustoma grandiflorum*
flavonol synthase. fls.

BAA20143.1 AB003779 *Perilla frutescens*
leucoanthocyanidin dioxygenase.

AAB66560.1 AF015885 *Callistephus chinensis*
anthocyanidin synthase.

BAB21477.1 AB044091 *Torenia fournieri*
anthocyanidin synthase. 2-oxoglutarate dependent oxygenase.

CAA63092.1 X92178 *Solanum tuberosum*
flavonol synthase.

AAD26261.1 AF119095 *Malus x domestica*
flavonol synthase. FLS.

CAA53580.1 X75966 *Vitis vinifera*
leucoanthocyanidin dioxygenase. LDOX.

BAA75305.1 AB023786 *Ipomoea batatas*
anthocyanidin synthase. ans I.

AAB84049.1 AF028602 *Ipomoea purpurea*
anthocyanidin synthase. ANS-FL1.

BAA75306.1 AB023787 *Ipomoea batatas*
anthocyanidin synthase. ans II.

CAA73094.1 Y12489 *Forsythia x intermedia*
anthocyanidin synthase.

CAA69252.1 Y07955 *Oryza sativa*
anthocyanidin synthase. ANS.

SEQ ID NO: 794

AAD10204.1 AF030260 *Vicia sativa*
CYP94A1. vagh111. cytochrome P450 fatty acid hydroxylase; Method: conceptual translation
with partial peptide sequencing.

AAG33645.1 AF092917 *Vicia sativa*
cytochrome P450-dependent fatty acid hydroxylase. CYP94A2.

AAG17470.1 AF123609 *Triticum aestivum*
cytochrome P450.

BAA99523.1 AP002484 *Oryza sativa*
putative cytochrome P450. P0489A01.14.

AAK31592.1 AY029178 *Brassica rapa* subsp. *pekinensis*
cytochrome P450. mf-CYP450. possible relevance to male-sterility.

BAA99522.1	AP002484	Oryza sativa putative cytochrome P450. P0489A01.13.
BAA83370.1	AP000391	Oryza sativa ESTs AU056036(S20239),C72753(E2173), AU056035(S20239) correspond to a region of the predicted gene.; Similar to putative cytochrome P-450 (AC003680).
CAB41474.1	AJ238402	Catharanthus roseus cytochrome P450. CYP96C1.
AAB94586.1	AF022457	Glycine max CYP97B2p. CYP97B2. cytochrome P450 monooxygenase.
AAK20054.1	AC025783	Oryza sativa putative cytochrome P450 monooxygenase. OSJNBA0001O14.16.
AAK38086.1	AF321862	Lolium rigidum putative cytochrome P450.
AAK38085.1	AF321861	Lolium rigidum putative cytochrome P450.
AAB94588.1	AF022459	Glycine max CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
CAA89260.1	Z49263	Pisum sativum cytochrome P450.
AAG09208.1	AF175278	Pisum sativum wound-inducible P450 hydroxylase. CYP82A1.
AAC49188.2	U29333	Pisum sativum cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
BAB19083.1	AP002744	Oryza sativa putative cytochrome P450. P0006C01.25. contains ESTs AU081507(C12518),C26520(C12518).
BAB19104.1	AP002839	Oryza sativa putative cytochrome P450. P0688A04.10. contains ESTs AU081507(C12518),C26520(C12518).
AAK38092.1	AF321868	Lolium rigidum putative cytochrome P450.
CAA04117.1	AJ000478	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11. chimeric sequence (from 5'-race).
AAK38091.1	AF321867	Lolium rigidum putative cytochrome P450.
CAA04116.1	AJ000477	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
BAA22423.1	AB001380	Glycyrrhiza echinata cytochrome P450. CYP93B1.
CAA71876.1	Y10982	Glycine max putative cytochrome P450.

BAB39252.1	AP002968	Oryza sativa putative cytochrome P450. P0416G11.1.
AAA33106.1	L10081	Catharanthus roseus cytochrome P-450 protein. CYP72. putative; CYP72 protein.
AAA17746.1	L19075	Catharanthus roseus cytochrome P450. CYP72C. putative.
BAA74466.1	AB022733	Glycyrhiza echinata cytochrome P450. CYP Ge-51.
BAB19121.1	AP002839	Oryza sativa putative cytochrome P450. P0688A04.28.
AAA17732.1	L19074	Catharanthus roseus cytochrome P450. CYP72B.
BAA93634.1	AB025016	Lotus japonicus cytochrome P450.
AAB05376.3	U35226	Nicotiana plumbaginifolia putative cytochrome P-450.
AAB61965.1	U48435	Solanum chacoense putative cytochrome P450.
AAF27282.1	AF122821	Capsicum annuum cytochrome P450. PepCYP.
CAB50768.1	AJ243804	Cicer arietinum putative isoflavone synthase. cytochrome P450. cyp93C3.
AAC34853.1	AF082028	Hemerocallis hybrid cultivar putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3. mRNA accumulates in senescing petals.
CAB43505.1	AJ239051	Cicer arietinum cytochrome P450. cyp81E2.
BAB21156.1	AP002899	Oryza sativa putative cytochrome P450. P0456A01.12.
CAA50648.1	X71657	Solanum melongena P450 hydroxylase.
BAB19112.1	AP002839	Oryza sativa putative cytochrome P450. P0688A04.18. contains ESTs AU067870(C10320),AU067869(C10320).
BAB19091.1	AP002744	Oryza sativa putative cytochrome P450. P0006C01.33. contains ESTs AU067870(C10320),AU067869(C10320).
BAA84072.1	AB028152	Torenia hybrida flavone synthase II. cytochrome P450. TFNS5.
BAA76380.1	AB023636	Glycyrhiza echinata cytochrome P450. CYP Ge-8.
CAA72208.1	Y11404	Zea mays cytochrome p450. cyp71c2.

CAA57423.1	X81829	Zea mays cytochrome P450. CYP71C2. family CYP71, subfamily CYP71C.
BAB12433.1	AB025030	Coptis japonica p450.
SEQ ID NO: 798		
BAB21205.1	AP002913	Oryza sativa nucleoid DNA-binding protein cnd41-like protein. P0480E02.11. contains ESTs AU166073(E31027),AU029516(E31027).
BAA22813.1 D26015 Nicotiana tabacum aspartic protease activity. CND41, chloroplast nucleoid DNA binding protein. cnd41.		
SEQ ID NO: 804		
AAD46491.1	AF135014	Zea mays dihydrolipoamide S-acetyltransferase. pyruvate dehydrogenase complex E2 subunit.
SEQ ID NO: 805		
BAA85412.1	AP000615	Oryza sativa ESTs AU065232(E60855),C23624(S1554), AU078241(E60855) correspond to a region of the predicted gene.; similar to putative adenylate kinase. (AC005896).
BAA01181.1	D10335	Oryza sativa adenylate kinase-b. Adk-b.
BAA01180.1	D10334	Oryza sativa adenylate kinase-a. Adk-a.
BAA94761.1	AB041773	Oryza sativa adenylate kinase. Adk-a.
AAB68604.1	U82330	Prunus armeniaca adenylate kinase homolog.
AAF23372.1	AF187063	Oryza sativa catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase b. ura6.
AAF23371.1	AF187062	Oryza sativa catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase a. ura6.
AAD41679.1	AF086603	Ceratopteris richardii adenylate kinase. ADK1.
BAA85443.1	AP000616	Oryza sativa similar to UMP/CMP kinase (AF000147).
SEQ ID NO: 808		
CAA41774.1	X59046	Oryza sativa sucrose-UDP glucosyltransferase (isozyme 2). RSs2.
BAA89049.1	AB029401	Citrus unshiu sucrose synthase. CitSUS1-2.
AAA34196.1	L19762	Lycopersicon esculentum sucrose synthase.

BAA88905.1	AB022092	Citrus unshiu sucrose synthase. CitSUS1.
AAD28641.1	U73588	Gossypium hirsutum sucrose synthase.
CAA49428.1	X69773	Vicia faba sucrose synthase. VfSucs.
AAC37346.1	M97551	Vicia faba cleavage of sucrose. UDP-glucose:D-fructose-2-glucosyltransferase. putative.
CAA09681.1	AJ011535	Lycopersicon esculentum sucrose synthase. sus2.
AAA97572.1	U24088	Solanum tuberosum sucrose synthase.
CAA09593.1	AJ011319	Lycopersicon esculentum sucrose synthase. sus3.
CAB40794.1	AJ131943	Medicago truncatula sucrose synthase. sucS1.
AAC17867.1	AF049487	Medicago sativa sucrose hydrolysis. sucrose synthase.
CAB40795.1	AJ131964	Medicago truncatula sucrose synthase. sucS1.
CAA65640.1	X96939	Tulipa gesneriana sucrose-synthase 21.
AAA97571.1	U24087	Solanum tuberosum sucrose synthase.
CAA63122.1	X92378	Alnus glutinosa sucrose synthase. sus1.
AAA33514.1	L22296	Zea mays UDP-glucose:D-fructose 2-glucosyl-transferase. Sus1.
CAA65639.1	X96938	Tulipa gesneriana sucrose-synthase 1.
AAC41682.1	L03366	Oryza sativa sucrose synthase 3. RSs3.
CAA75793.1	Y15802	Hordeum vulgare sucrose synthase 2. Ss2.
CAA49551.1	X69931	Hordeum vulgare sucrose synthase. Ss2.
CAA76056.1	Y16090	Daucus carota sucrose synthase isoform I. Susy*Dcl1.
CAA53081.1	X75332	Daucus carota sucrose synthase.
AAA33515.1	L33244	Zea mays sucrose synthase 2. Sus1.

BAB20799.1 AB045710 *Pyrus pyrifolia*
sucrose synthase 1. PypSUS1.

CAA03935.1 AJ000153 *Triticum aestivum*
sucrose synthase type 2.

AAC39323.1 AF030231 *Glycine max*
sucrose synthase. SS. nodulin-100.

BAA01108.1 D10266 *Vigna radiata*
sucrose synthase. vss1.

CAA09910.1 AJ012080 *Pisum sativum*
sucrose synthase.

AAC28107.1 AF079851 *Pisum sativum*
nodule-enhanced sucrose synthase. ness.

CAC32462.1 AJ311496 *Pisum sativum*
sucrose metabolism. sucrose synthase isoform 3. sus3.

CAA57881.1 X82504 *Chenopodium rubrum*
sucrose synthase. CSS1.

CAA26229.1 X02382 *Zea mays*
sucrose synthase.

CAA26247.1 X02400 *Zea mays*
sucrose synthase.

CAA46017.1 X64770 *Oryza sativa*
sucrose synthase. RSs1.

CAB38022.1 AJ132000 *Craterostigma plantagineum*
sucrose metabolism. sucrose synthase. Ss2.

CAA78747.1 Z15028 *Oryza sativa*
sucrose synthase.

AAF85966.1 AF263384 *Saccharum officinarum*
sucrose synthase-1.

CAA46701.1 X65871 *Hordeum vulgare*
sucrose synthase.

CAA04543.1 AJ001117 *Triticum aestivum*
sucrose synthase type I. Ss1.

BAA88904.1 AB022091 *Citrus unshiu*
sucrose synthase. CitSUSA.

BAA88981.1 AB025778 *Citrus unshiu*
sucrose synthase. CitSUSA-2.

CAA04512.1 AJ001071 *Pisum sativum*
second sucrose synthase.

CAA76057.1 Y16091 *Daucus carota*
sucrose synthase isoform II. Susy*Dc2.

CAB38021.1 AJ131999 *Craterostigma plantagineum*
sucrose metabolism. sucrose synthase. Ss1.

CAA57499.1 X81974 Beta vulgaris
sucrose synthase. SBSS1.

CAA47264.1 X66728 Hordeum vulgare
sucrose synthase.

SEQ ID NO: 809

AAB69317.1 AF012861 Petroselinum crispum
plastidic glucose-6-phosphate dehydrogenase. pG6PDH.

AAF87216.1 AF231351 Nicotiana tabacum
plastidic glucose 6-phosphate dehydrogenase. G6PDHP2.

CAA67782.1 X99405 Nicotiana tabacum
glucose-6-phosphate dehydrogenase. G6PD.

CAB52708.1 AJ010712 Solanum tuberosum
glucose-6-phosphate 1-dehydrogenase. g6pd.

CAB52685.1 AJ132346 Dunaliella bioculata
plastidic glucose-6-phosphate dehydrogenase. g6PD.

CAA58775.1 X83923 Solanum tuberosum
glucose-6-phosphate dehydrogenase.

CAA03941.1 AJ000184 Spinacia oleracea
Glucose-6-phosphate dehydrogenase. G6PD.

CAA03939.1 AJ000182 Spinacia oleracea
Glucose-6-phosphate dehydrogenase. G6PD.

CAA04994.1 AJ001772 Nicotiana tabacum
glucose-6-phosphate dehydrogenase. TCG18.

CAA03940.1 AJ000183 Spinacia oleracea
Glucose-6-phosphate dehydrogenase. G6PD.

AAD11426.1 AF097663 Mesembryanthemum crystallinum
cytoplasmic glucose-6-phosphate 1-dehydrogenase. G6PD.

AAB41552.1 U18238 Medicago sativa subsp. sativa
glucose-6-phosphate dehydrogenase.

CAA52442.1 X74421 Solanum tuberosum
glucose-6-phosphate 1-dehydrogenase. g6pdh. homotetramer.

AAB69318.1 AF012862 Petroselinum crispum
cytosolic glucose-6-phosphate dehydrogenase 1. cG6PDH1.

AAB69319.1 AF012863 Petroselinum crispum
cytosolic glucose-6-phosphate dehydrogenase 2. cG6PDH2.

CAA04992.1 AJ001769 Nicotiana tabacum
glucose-6-phosphate dehydrogenase. TCG6.

CAA04993.1 AJ001770 Nicotiana tabacum
glucose-6-phosphate dehydrogenase. TCG9.

BAA97662.1 AB029454 Triticum aestivum
glucose-6-phosphate dehydrogenase. g6pdh.

BAA97663.1 AB029455 *Triticum aestivum*
glucose-6-phosphate dehydrogenase. g6pdh.

BAA97664.1 AB029456 *Triticum aestivum*
glucose-6-phosphate dehydrogenase. g6pdh.

AAG23802.1 AF260736 *Cucurbita pepo*
plastidic glucose-6-phosphate dehydrogenase.

CAB66330.1 AJ279688 *Betula pendula*
glucose-6-phosphate dehydrogenase. g6pd.

BAA82155.1 AB011441 *Triticum aestivum*
glucose-6-phosphate dehydrogenase. WESR5. salt-stress responding gene.

CAA06200.1 AJ004900 *Glycine max*
pentose phosphate pathway oxidoreductase generating NADPH. glucose-6-phosphate-
dehydrogenase.

SEQ ID NO: 812

BAA08910.1 D50407 *Cucumis sativus*
glutamyl-tRNA reductase. hemA.

AAD16897.1 AF105221 *Glycine max*
converts glutamyl-tRNA to glutamate 1-semialdehyde. glutamyl-tRNA reductase precursor.
gtr1.

BAA11091.1 D67088 *Cucumis sativus*
glutamyl-tRNA reductase. hemA2.

BAA25003.1 AB011416 *Oryza sativa*
glutamyl-tRNA reductase.

AAG13620.1 AC078840 *Oryza sativa*
putative glutamyl-tRNA reductase. OSJNBb0073N24.1.

CAA60054.1 X86101 *Hordeum vulgare*
aminolevulinate synthesis (chlorophyll synthesis). glutamyl tRNA reductase. hemA 1. 1st
isoform.

CAA63140.1 X92403 *Hordeum vulgare*
glutamyl-tRNA reductase. hemA1. isoform I.

BAA25167.1 D88382 *Hordeum vulgare*
glutamyl-tRNA reductase. hemA1. isoform 1.

CAA60055.1 X86102 *Hordeum vulgare*
aminolevulinate synthesis (chlorophyll synthesis). glutamyl tRNA reductase. hemA 2. 2nd
isoform.

BAA25168.1 D88383 *Hordeum vulgare*
glutamyl-tRNA reductase. hemA3. isoform 3.

AAG41962.1 AF305613 *Chlamydomonas reinhardtii*
glutamyl-tRNA reductase precursor. HemA. pGtr.

AAG02480.1 AF294753 *Hordeum vulgare*
converts glutamyl-tRNA to glutamate 1-semialdehyde in the chlorophyll biosynthetic
pathway. glutamyl-tRNA reductase. hemA2.

AAG02479.1 AF294752 *Hordeum vulgare*
 converts glutamyl-tRNA to glutamate 1-semialdehyde in the chlorophyll biosynthetic pathway. glutamyl-tRNA reductase. hemA1.

SEQ ID NO: 813

BAA82556.1 AB030083 *Populus nigra*
 lectin-like protein kinase. PnLPK.

AAD21872.1 AF078082 *Phaseolus vulgaris*
 receptor-like protein kinase homolog RK20-1.

AAF43408.1 AF230515 *Oryza sativa* subsp. *japonica*
 serine/threonine protein kinase. YK35.

CAB51480.1 Y14600 *Sorghum bicolor*
 putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

CAA73134.1 Y12531 *Brassica oleracea*
 serine/threonine kinase. BRLK.

AAB93834.1 U82481 *Zea mays*
 KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

AAK00425.1 AC069324 *Oryza sativa*
 Putative protein kinase. OSJNBa0071K19.11.

BAA92954.1 AP001551 *Oryza sativa*
 Similar to *Oryza sativa* protein kinase (OSPK10) mRNA. (L27821).

BAB39873.1 AP002882 *Oryza sativa*
 putative protein kinase. P0439B06.8. contains ESTs
 AU056701(S20808),AU056702(S20808).

BAB19337.1 AP003044 *Oryza sativa*
 putative protein kinase. P0038C05.10. contains ESTs
 AU056335(S20481),AU056336(S20481).

AAK21965.1 AY028699 *Brassica napus*
 receptor protein kinase PERK1.

BAA92953.1 AP001551 *Oryza sativa*
 Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).

BAB07906.1 AP002835 *Oryza sativa*
 putative S-receptor kinase. P0417G05.14.

BAA94516.1 AP001800 *Oryza sativa*
 Similar to *Zea mays* S-domain receptor-like protein kinase (AJ010166).

AAD52097.1 AF088885 *Nicotiana tabacum*
 receptor-like kinase CHRK1. Chrk1.

BAB21240.1 AP002953 *Oryza sativa*
 Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).

AAC23542.1 U20948 *Ipomoea trifida*
 receptor protein kinase. IRK1.

BAB18292.1	AP002860	Oryza sativa putative receptor-like protein kinase. P0409B08.19.
AAG16628.1	AY007545	Brassica napus protein serine/threonine kinase BNK1.
AAA33915.1	L27821	Oryza sativa receptor type serine/threonine kinase. protein kinase.
BAB03429.1	AP002817	Oryza sativa EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAA94509.1	AB041503	Populus nigra protein kinase 1. PnPK1.
AAD46420.1	AF100771	Hordeum vulgare receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
AAD38286.1	AC007789	Oryza sativa putative protein kinase. OSJNBa0049B20.13.
BAB40081.1	AP003074	Oryza sativa putative receptor protein kinase. OSJNBa0004G10.30.
BAB18321.1	AP002865	Oryza sativa putative receptor protein kinase. P0034C11.11.
BAA94517.1	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA21132.1	D88193	Brassica rapa S-receptor kinase. SRK9 (B.c.).
BAA06285.1	D30049	Brassica rapa S-receptor kinase SRK9.
BAB07905.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.13.
BAA94529.2	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
AAB61708.1	U93048	Daucus carota somatic embryogenesis receptor-like kinase. SERK.
CAA79355.1	Z18921	Brassica oleracea S-receptor kinase-like protein.
AAK11674.1	AF339747	Lophopyrum elongatum protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.

BAA94528.1	AP001800	Oryza sativa
Similar to Arabidopsis thaliana chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).		
BAA94510.1	AB041504	Populus nigra
		protein kinase 2. PnPK2.
AAA33000.1	M76647	Brassica oleracea
		receptor protein kinase. SKR6.
CAA67145.1	X98520	Brassica oleracea
		receptor-like kinase. SFR2.
AAB47421.1	U59316	Lycopersicon esculentum
		serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
BAA07577.2	D38564	Brassica rapa
		receptor protein kinase SRK12.
AAA33008.1	M97667	Brassica napus
		serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus
		ser /thr kinase. S-locus receptor kinase. srk.
BAA92837.1	AB032474	Brassica oleracea
		S60 S-locus receptor kinase. SRK60.

SEQ ID NO: 814

AAF23903.1	AF194416	Oryza sativa
MAP kinase homolog. MAPK2. RMAPK2.		
AAD52659.1	AF177392	Oryza sativa
blast and wounding induced mitogen-activated protein kinase. BWMK1. BWMK1 MAP kinase.		
AAF23902.1	AF194415	Oryza sativa
		MAP kinase homolog. MAPK1. RMAPK1.
AAD28617.1	AF129087	Medicago sativa
		mitogen-activated protein kinase homologue. TDY1.
CAB61750.1	AJ275316	Cicer arietinum
		MAP kinase protein.
AAB57843.1	U96716	Selaginella lepidophylla
		MAP kinase-like protein. sdhn-6r.
AAF65766.1	AF242308	Euphorbia esula
		mitogen-activated protein kinase. regulated by tyrosine and threonine phosphorylation.
BAB18271.1	AB035141	Chlamydomonas reinhardtii
		mitogen-activated protein kinase. CrMPK2.
CAA58761.1	X83880	Nicotiana tabacum
		p45Ntf4 serine/threonine protein kinase. ntf4.
CAA47099.1	X66469	Medicago sativa
		MAP Kinase. MSK7.

AAB41548.1 L07042 *Medicago sativa*
autophosphorylating serine/threonine protein kinase. MAP kinase. MsERK1.

AAB58396.1 U94192 *Nicotiana tabacum*
salicylic acid-activated MAP kinase. NtSIPK.

CAA50036.1 X70703 *Pisum sativum*
MAP kinase homologue. PSMAPKIN.

AAF73236.1 AF153061 *Pisum sativum*
MAP kinase 3. Mapk3. PsMAPK3.

BAB32406.1 AB055515 *Nicotiana tabacum*
NRK1 MAPK. nrk1. A tobacco MAPK that is phosphorylated and activated by NQK1.

CAA58760.1 X83879 *Nicotiana tabacum*
p43Nft6 serine/threonine protein kinase. ntf6.

CAA57721.1 X82270 *Medicago sativa*
protein kinase. MMK4.

AAF81420.1 AF247136 *Capsicum annuum*
MAP kinase 2. MK2. CAMK2; wound, UV-C, and cold-inducible expression.

AAD37790.1 AF149424 *Ipomoea batatas*
MAP kinase.

AAG40580.1 AF216316 *Oryza sativa*
MAP kinase 2. protein kinase; MAP2.

CAB37188.1 AJ224336 *Medicago sativa*
MAP kinase. MMK3.

AAF61238.1 AF241166 *Oryza sativa*
MAP kinase MAPK2.

AAG40581.1 AF216317 *Oryza sativa*
MAP kinase 3. protein kinase; MAP3.

CAB61889.1 AJ251330 *Oryza sativa*
protein kinase. MAPK4 protein. mapk4.

CAA73323.1 Y12785 *Petroselinum crispum*
MAP kinase I.

CAC13967.1 AJ250311 *Oryza sativa*
protein kinase. MAPK2 protein. mapk2.

CAA56314.1 X79993 *Avena sativa*
MAP KINASE. Asmap1.

CAA49592.1 X69971 *Nicotiana tabacum*
serine/threonine protein kinase. NTF3.

CAA58466.1 X83440 *Petunia x hybrida*
MAP/ERK kinase 1. MEK1.

AAK01710.1 AF332873 *Oryza sativa*
MAP kinase BIMK1.

AAG40579.1 AF216315 *Oryza sativa*
MAP kinase 1. protein kinase; MAP1.

CAA57719.1	X82268	Medicago sativa protein kinase. MMK2.
AAC28850.1	AF079318	Triticum aestivum protein kinase. MAP kinase homolog. WCK-1.
AAD32204.1	AF134730	Prunus armeniaca putative mitogen-activated protein kinase MAPK. MAP kinase.
BAA74734.1	AB016802	Zea mays MAP kinase 5. ZmMPK5.
AAF73257.1	AF154329	Pisum sativum MAP kinase PsMAPK2. Mapk2.
BAA09600.1	D61377	Nicotiana tabacum WIPK. MAP (mitogen-activated protein) kinase.
AAF81419.1	AF247135	Capsicum annuum MAP kinase 1. MK1. wound and UV-C inducible expression.
BAA74733.1	AB016801	Zea mays MAP kinase 4. ZmMPK4.
CAA05328.1	AJ002314	Nicotiana tabacum serine/threonine protein kinase. shaggy-like kinase 111. NSK 111.
CAA05329.1	AJ002315	Nicotiana tabacum shaggy-like kinase 59. NSK 59.
CAA11861.1	AJ224164	Petunia x hybrida shaggy kinase 6. PSK6.
CAA58595.1	X83620	Petunia x hybrida Petunia Shaggy kinase 6. PSK6.
CAA11862.1	AJ224165	Petunia x hybrida shaggy kinase 7. PSK7.
CAA58594.1	X83619	Petunia x hybrida Petunia Shaggy kinase 4. PSK4.
AAA92823.1	U18365	Brassica napus cyclin dependent protein kinase homolog; similar to moth bean p34cdc2 protein, PIR Accession Number JQ2243.
BAA92214.1	AP001278	Oryza sativa ESTs C22403(C50132),C22404(C50132) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana shaggy related protein kinase ASK-gamma. (P43289).
CAA67554.1	X99100	Trifolium repens protein kinase. trK.
SEQ ID NO: 816		
CAA65065.1	X95759	Solanum tuberosum glycogen (starch) synthase.
CAA64173.1	X94400	Solanum tuberosum soluble-starch-synthase. SSSIII.

AAC14014.1 AF023159 *Zea mays*
starch synthase DULL1. dull1. similar to potato starch synthase SSIII; likely to be the maize starch synthase defined biochemically as SSII.

CAB40374.1 AJ225088 *Vigna unguiculata*
ADP-glucose-starch glucosyltransferase. Starch synthase isoform SS III.

AAF88000.1 AF258609 *Aegilops tauschii*
starch synthase III.

AAF87999.1 AF258608 *Triticum aestivum*
starch synthase III. wSSIII.

CAB40375.1 AJ006752 *Vigna unguiculata*
ADP-glucose starch glucosyltransferase. starch synthase, isoform V.

AAC14015.1 AF023160 *Zea mays*
starch synthase DULL1. dull1. similar to potato starch synthase SSIII; like to be the maize starch synthase defined biochemically as SSII.

AAC17971.2 AF026422 *Chlamydomonas reinhardtii*
soluble starch synthase. ADP-glucose:alpha-1, 4-D-glucan-4-alpha-D-glucosyltransferase.

AAD13342.1 AF019297 *Zea mays*
starch synthase isoform zSTSII-2. zSSIIb.

CAB86618.1 AJ269502 *Triticum aestivum*
transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-1. wSs2a-1.

CAA61269.1 X88790 *Pisum sativum*
glycogen (starch) synthase.

CAB96626.1 AJ269503 *Triticum aestivum*
transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-2. wSs2a-2.

CAB96627.1 AJ269504 *Triticum aestivum*
transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-3. wSs2a-3.

CAA71442.1 Y10416 *Solanum tuberosum*
soluble starch (bacterial glycogen) synthase. SS I.

AAD53263.1 AF155217 *Triticum aestivum*
starch synthase IIa.

AAF37876.1 AF234163 *Hordeum vulgare*
starch synthase I. SSI.

CAB99209.1 AJ292521 *Triticum aestivum*
essential for starch synthesis. starch synthase I-1. wSsI-1.

AAD54661.1 AF091803 *Triticum aestivum*
starch synthase I.

AAB17085.1 U66377 *Triticum aestivum*
starch synthase. TaSS. EC 2.4.1.11.

CAB99210.1 AJ292522 *Triticum aestivum*
essential for starch synthesis. starch synthase I-2. wSsI-2.

AAF03557.1	AF091802	<i>Aegilops tauschii</i> starch synthase I.
AAD13341.1	AF019296	<i>Zea mays</i> starch synthase isoform zSTSII-1. zSSIIa.
AAC17969.2	AF026420	<i>Chlamydomonas reinhardtii</i> ADP-Glucose:alpha-1, 4-D-glucan-4-alpha-D-glucosyltransferase. granule-bound starch synthase I precursor. STA2. GBSSI.
BAA82346.1	AB029546	<i>Phaseolus vulgaris</i> granule-bound starch synthase I. GBSSI.
CAA37732.1	X53694	<i>Oryza sativa</i> starch synthase.
CAA52273.1	X74160	<i>Manihot esculenta</i> starch (bacterial glycogen) synthase. GBSS.
AAF72561.1	AF141954	<i>Oryza sativa</i> granule-bound starch synthase. Waxy.
CAA46294.1	X65183	<i>Oryza sativa</i> glycogen (starch) synthase. waxy gene. starch granule enzyme.
AAF72562.1	AF141955	<i>Oryza sativa</i> granule-bound starch synthase. Waxy.
CAA44065.1	X62134	<i>Oryza sativa</i> starch biosynthesis. starch (bacterial glycogen) synthase. Wx.
AAB02197.1	U48227	<i>Triticum aestivum</i> soluble starch synthase.
AAF13168.1	AF173900	<i>Manihot esculenta</i> granule bound starch synthase II precursor. GBSSII. MEGBSSII.
CAA45472.1	X64108	<i>Oryza sativa</i> starch granule-bound starch synthase. waxy.
AAC61675.2	AF031162	<i>Oryza sativa</i> granule-bound starch synthase. Waxy.
AAC70779.1	AF097922	<i>Astragalus membranaceus</i> granule-bound glycogen (starch) synthase. GBSS.
CAA06958.1	AJ006293	<i>Antirrhinum majus</i> granule-bound starch synthase. waxy.
AAC19119.1	AF068834	<i>Ipomoea batatas</i> starch synthase.
AAD49850.1	AF165890	<i>Oryza sativa</i> subsp. <i>japonica</i> soluble starch synthase.
BAA81848.1	AB026295	<i>Oryza sativa</i> ESTs AU075322(C11109),D22430(C11109) correspond to a region of the predicted gene.; Rice gene for soluble starch synthase (SSS1), complete cds (exon1-15).(D38221).
BAA03739.1	D16202	<i>Oryza sativa</i> soluble starch synthase precursor.

CAA61268.1	X88789	Pisum sativum glycogen (starch) synthase.
AAA86423.1	U44126	Ipomoea batatas starch synthase. SPSS67.
AAF14233.1	AF109395	Triticum aestivum granule-bound starch synthase GBSSII.
CAA41359.1	X58453	Solanum tuberosum glycogen (starch) synthase. amf. waxy protein, granule-bound starch synthase.
AAG43519.1	AF210699	Perilla frutescens granule-bound starch synthase. GBSSI. waxy protein.
SEQ ID NO: 819		
BAA13032.1	D86180	Pisum sativum phosphoribosylanthranilate transferase. PAT1.
SEQ ID NO: 822		
AAB86850.1	AF031540	Fritillaria agrestis cytochrome C. cytC.
AAC84135.1	AF101422	Cichorium intybus cytochrome.
BAA02159.1	D12634	Oryza sativa 'cytochrome C'.
AAA63515.1	M63704	Oryza sativa cytochrome c. Cc-1.
AAA92712.1	L77113	Helianthus annuus cytochrome c. cytc1. putative.
AAB70265.1	AF017367	Oryza sativa cytochrome C.
AAA33084.1	M35173	Chlamydomonas reinhardtii apocytochrome c (cyc).
CAB16954.1	Z99829	Chlamydomonas reinhardtii cytochrome c. CYC1.
CAA79708.1	Z21499	Stellaria longipes mitochondrial cytochrome c.
SEQ ID NO: 823		
BAA02159.1	D12634	Oryza sativa 'cytochrome C'.
AAA63515.1	M63704	Oryza sativa cytochrome c. Cc-1.
AAB86850.1	AF031540	Fritillaria agrestis cytochrome C. cytC.
AAC84135.1	AF101422	Cichorium intybus cytochrome.

AAA92712.1 L77113 Helianthus annuus
cytochrome c. cytcl. putative.

AAB70265.1 AF017367 Oryza sativa
cytochrome C.

AAA33084.1 M35173 Chlamydomonas reinhardtii
apocytochrome c (cyc).

CAB16954.1 Z99829 Chlamydomonas reinhardtii
cytochrome c. CYC1.

CAA79708.1 Z21499 Stellaria longipes
mitochondrial cytochrome c.

SEQ ID NO: 825

BAB17113.1 AP002866 Oryza sativa
putative white protein; ATP-binding cassette transporter. P0410E01.34.

AAF43869.1 AF166114 Chloroplast Mesostigma viride
probable transport protein. cysA.

BAA90508.1 AP001111 Oryza sativa
similar to ABC transporter of Arabidopsis thaliana (AC004697).

AAD54843.1 AF137379 Chloroplast Nephroselmis olivacea
probable transport protein. cysA.

BAA57907.1 AB001684 Chlorella vulgaris
sulfate transport system permease protein. cysA.

BAA90507.1 AP001111 Oryza sativa
similar to ABC transporter of Arabidopsis thaliana (AC004697).

BAB40032.1 AP003046 Oryza sativa
putative ABC transporter. P0445D12.3.

AAG49003.1 AY013246 Hordeum vulgare
putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and
comparative sequence.

BAB21275.1 AP002844 Oryza sativa
putative ABC transporter protein. P0410E03.6.

AAG45492.1 AY013245 Oryza sativa
36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and
comparative sequence.

AAG49002.1 AY013246 Hordeum vulgare
putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative
sequencing.

BAB21276.1 AP002844 Oryza sativa
putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).

AAD10836.1 U52079 Solanum tuberosum
P-glycoprotein. pmdrl. binds ATP; ATPase; transporter; transmembrane protein.

BAB21279.1 AP002844 Oryza sativa
putative ABC transporter protein. P0410E03.10. contains ESTs
AU065360(R3463), AU101680(R3463).

BAB21273.1 AP002844 Oryza sativa putative ABC transporter protein. P0410E03.4.
BAA83352.1 AP000391 Oryza sativa ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.; Similar to ABC transporter-7 (U43892).
BAA96612.1 AP002482 Oryza sativa Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ; putative ABC transporter (AC004411).
SEQ ID NO: 827
AAG34803.1 AF243368 Glycine max glutathione S-transferase GST 13.
AAG16758.1 AY007560 Lycopersicon esculentum putative glutathione S-transferase T3.
AAG34798.1 AF243363 Glycine max glutathione S-transferase GST 8.
AAF64450.1 AF239928 Euphorbia esula glutathione S-transferase. similar to auxin-inducible GST.
AAG34807.1 AF243372 Glycine max glutathione S-transferase GST 17.
AAG34796.1 AF243361 Glycine max glutathione S-transferase GST 6.
AAG16759.1 AY007561 Lycopersicon esculentum putative glutathione S-transferase T4.
AAG34797.1 AF243362 Glycine max glutathione S-transferase GST 7.
AAG34801.1 AF243366 Glycine max glutathione S-transferase GST 11.
AAG34804.1 AF243369 Glycine max glutathione S-transferase GST 14.
AAG34809.1 AF243374 Glycine max glutathione S-transferase GST 19.
AAG34808.1 AF243373 Glycine max glutathione S-transferase GST 18.
AAG34810.1 AF243375 Glycine max glutathione S-transferase GST 20.
AAG16757.1 AY007559 Lycopersicon esculentum putative glutathione S-transferase T2.
AAG16756.1 AY007558 Lycopersicon esculentum putative glutathione S-transferase T1.
AAG34844.1 AF244701 Zea mays glutathione S-transferase GST 36.
AAG34805.1 AF243370 Glycine max glutathione S-transferase GST 15.

AAG34831.1 AF244688 Zea mays
glutathione S-transferase GST 23.

AAG34832.1 AF244689 Zea mays
glutathione S-transferase GST 24.

AAG34849.1 AF244706 Zea mays
glutathione S-transferase GST 41.

AAG34802.1 AF243367 Glycine max
glutathione S-transferase GST 12.

CAA09187.1 AJ010448 Alopecurus myosuroides
glutathione transferase. GST1a.

AAG34829.1 AF244686 Zea mays
glutathione S-transferase GST 21.

CAA09188.1 AJ010449 Alopecurus myosuroides
glutathione transferase. GST1b.

AAA68430.1 J03679 Solanum tuberosum
glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.

AAG34836.1 AF244693 Zea mays
glutathione S-transferase GST 28.

AAG34837.1 AF244694 Zea mays
glutathione S-transferase GST 29.

AAG34800.1 AF243365 Glycine max
glutathione S-transferase GST 10.

AAC18566.1 AF048978 Glycine max
2,4-D inducible glutathione S-transferase. GSTa.

AAC32118.1 AF051214 Picea mariana
probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione
S-transferase encoded by GenBank Accession Number X56266.

AAF22517.1 AF118924 Papaver somniferum
glutathione S-transferase 1. GST1.

AAF22518.1 AF118925 Papaver somniferum
glutathione S-transferase 2. GST2.

AAG32471.1 AF309378 Oryza sativa subsp. japonica
putative glutathione S-transferase OsGSTU4.

AAG34806.1 AF243371 Glycine max
glutathione S-transferase GST 16.

CAA04391.1 AJ000923 Carica papaya
glutathione transferase. PGST1.

AAG32472.1 AF309379 Oryza sativa subsp. japonica
putative glutathione S-transferase OsGSTU3.

AAG34833.1 AF244690 Zea mays
glutathione S-transferase GST 25.

CAA71784.1 Y10820 Glycine max
glutathione transferase.

AAG34847.1 AF244704 Zea mays
glutathione S-transferase GST 39.

AAF22519.1 AF118926 Papaver somniferum
glutathione S-transferase 3. GST3.

SEQ ID NO: 828

AAG34803.1 AF243368 Glycine max
glutathione S-transferase GST 13.

AAG34797.1 AF243362 Glycine max
glutathione S-transferase GST 7.

AAG34798.1 AF243363 Glycine max
glutathione S-transferase GST 8.

AAF64450.1 AF239928 Euphorbia esula
glutathione S-transferase. similar to auxin-inducible GST.

AAG16758.1 AY007560 Lycopersicon esculentum
putative glutathione S-transferase T3.

AAG34796.1 AF243361 Glycine max
glutathione S-transferase GST 6.

AAG16759.1 AY007561 Lycopersicon esculentum
putative glutathione S-transferase T4.

AAG34801.1 AF243366 Glycine max
glutathione S-transferase GST 11.

AAG34804.1 AF243369 Glycine max
glutathione S-transferase GST 14.

AAG34807.1 AF243372 Glycine max
glutathione S-transferase GST 17.

AAG34809.1 AF243374 Glycine max
glutathione S-transferase GST 19.

AAG34810.1 AF243375 Glycine max
glutathione S-transferase GST 20.

AAG16757.1 AY007559 Lycopersicon esculentum
putative glutathione S-transferase T2.

AAG16756.1 AY007558 Lycopersicon esculentum
putative glutathione S-transferase T1.

AAG34802.1 AF243367 Glycine max
glutathione S-transferase GST 12.

AAG34808.1 AF243373 Glycine max
glutathione S-transferase GST 18.

AAG34844.1 AF244701 Zea mays
glutathione S-transferase GST 36.

CAA09188.1 AJ010449 Alopecurus myosuroides
glutathione transferase. GST1b.

CAA09187.1 AJ010448	Alopecurus myosuroides glutathione transferase. GST1a.
AAG32472.1 AF309379	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU3.
AAA68430.1 J03679	Solanum tuberosum glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.
AAG34837.1 AF244694	Zea mays glutathione S-transferase GST 29.
AAG34800.1 AF243365	Glycine max glutathione S-transferase GST 10.
AAG34831.1 AF244688	Zea mays glutathione S-transferase GST 23.
AAC32118.1 AF051214	Picea mariana probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAG34805.1 AF243370	Glycine max glutathione S-transferase GST 15.
AAC18566.1 AF048978	Glycine max 2,4-D inducible glutathione S-transferase. GSTa.
AAG34829.1 AF244686	Zea mays glutathione S-transferase GST 21.
CAA04391.1 AJ000923	Carica papaya glutathione transferase. PGST1.
CAA71784.1 Y10820	Glycine max glutathione transferase.
AAG34795.1 AF243360	Glycine max glutathione S-transferase GST 5.
AAG34836.1 AF244693	Zea mays glutathione S-transferase GST 28.
AAG34832.1 AF244689	Zea mays glutathione S-transferase GST 24.
AAG34833.1 AF244690	Zea mays glutathione S-transferase GST 25.
AAG34849.1 AF244706	Zea mays glutathione S-transferase GST 41.
AAG34806.1 AF243371	Glycine max glutathione S-transferase GST 16.
CAA09189.1 AJ010450	Alopecurus myosuroides glutathione transferase. GST1c.
SEQ ID NO: 829	
AAG34803.1 AF243368	Glycine max glutathione S-transferase GST 13.

AAF64450.1 AF239928 *Euphorbia esula*
glutathione S-transferase, similar to auxin-inducible GST.

AAG16758.1 AY007560 *Lycopersicon esculentum*
putative glutathione S-transferase T3.

AAG34798.1 AF243363 *Glycine max*
glutathione S-transferase GST 8.

AAG34801.1 AF243366 *Glycine max*
glutathione S-transferase GST 11.

AAG34797.1 AF243362 *Glycine max*
glutathione S-transferase GST 7.

AAG34796.1 AF243361 *Glycine max*
glutathione S-transferase GST 6.

AAG34807.1 AF243372 *Glycine max*
glutathione S-transferase GST 17.

AAG16759.1 AY007561 *Lycopersicon esculentum*
putative glutathione S-transferase T4.

AAG34804.1 AF243369 *Glycine max*
glutathione S-transferase GST 14.

AAG34810.1 AF243375 *Glycine max*
glutathione S-transferase GST 20.

AAG34809.1 AF243374 *Glycine max*
glutathione S-transferase GST 19.

AAG16757.1 AY007559 *Lycopersicon esculentum*
putative glutathione S-transferase T2.

AAG16756.1 AY007558 *Lycopersicon esculentum*
putative glutathione S-transferase T1.

AAG34805.1 AF243370 *Glycine max*
glutathione S-transferase GST 15.

AAC18566.1 AF048978 *Glycine max*
2,4-D inducible glutathione S-transferase. GSTa.

AAG34808.1 AF243373 *Glycine max*
glutathione S-transferase GST 18.

AAG34800.1 AF243365 *Glycine max*
glutathione S-transferase GST 10.

AAG34829.1 AF244686 *Zea mays*
glutathione S-transferase GST 21.

AAG34802.1 AF243367 *Glycine max*
glutathione S-transferase GST 12.

AAG34837.1 AF244694 *Zea mays*
glutathione S-transferase GST 29.

CAA09187.1 AJ010448 *Alopecurus myosuroides*
glutathione transferase. GST1a.

CAA09188.1 AJ010449	Alopecurus myosuroides glutathione transferase. GST1b.
AAG34849.1 AF244706	Zea mays glutathione S-transferase GST 41.
AAG34844.1 AF244701	Zea mays glutathione S-transferase GST 36.
AAG34806.1 AF243371	Glycine max glutathione S-transferase GST 16.
CAA71784.1 Y10820	Glycine max glutathione transferase.
AAA68430.1 J03679	Solanum tuberosum glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.
CAA04391.1 AJ000923	Carica papaya glutathione transferase. PGST1.
AAG34836.1 AF244693	Zea mays glutathione S-transferase GST 28.
AAG34831.1 AF244688	Zea mays glutathione S-transferase GST 23.
AAG34847.1 AF244704	Zea mays glutathione S-transferase GST 39.
AAC32118.1 AF051214	Picea mariana probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAF29773.1 AF159229	Gossypium hirsutum glutathione S-transferase. GST.
AAG32472.1 AF309379	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU3.
AAG41204.1 AF321437	Suaeda maritima glutathione transferase.
CAC24549.1 AJ296343	Cichorium intybus x Cichorium endivia glutathione S-transferase. chi-GST1. auxin-induced GST.
SEQ ID NO: 830	
AAD37699.1 AF145730	Oryza sativa homeodomain leucine zipper protein. Oshox6. transcription factor.
BAA93461.1 AB028073	Physcomitrella patens homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.
AAF01765.1 AF184278	Glycine max homeodomain-leucine zipper protein 57. Hdl57. transcription factor.
AAF01764.2 AF184277	Glycine max homeodomain-leucine zipper protein 56. Hdl56. transcription factor.
BAA93466.1 AB028078	Physcomitrella patens homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.

CAB67118.1	Y17306	<i>Lycopersicon esculentum</i> homeodomain protein. h52.
AAF73482.1	AF268422	<i>Brassica rapa</i> subsp. <i>pekinensis</i> hb-6-like protein. transcription factor; similar to <i>Arabidopsis thaliana</i> hb-6 protein.
AAD37697.1	AF145728	<i>Oryza sativa</i> homeodomain leucine zipper protein. Oshox4. transcription factor.
BAA21017.1	D26578	<i>Daucus carota</i> transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.
BAA05624.1	D26575	<i>Daucus carota</i> transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.
BAA93460.1	AB028072	<i>Physcomitrella patens</i> homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.
BAA93464.1	AB028076	<i>Physcomitrella patens</i> homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.
BAA93467.1	AB028079	<i>Physcomitrella patens</i> homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.
BAA93465.1	AB028077	<i>Physcomitrella patens</i> homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.
BAA05625.1	D26576	<i>Daucus carota</i> transcriptiional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.
BAA93468.1	AB028080	<i>Physcomitrella patens</i> homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.
BAA05623.1	D26574	<i>Daucus carota</i> tranciptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.
BAA05622.1	D26573	<i>Daucus carota</i> transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.
AAD37698.1	AF145729	<i>Oryza sativa</i> homeodomain leucine zipper protein. Oshox5. transcription factor.
CAA64221.1	X94449	<i>Pimpinella brachycarpa</i> transcription activator. homeobox-leucine zipper protein. PHZ4.
CAA64152.1	X94375	<i>Pimpinella brachycarpa</i> transcription activator. homeobox-leucine zipper protein.
CAA64491.1	X95193	<i>Pimpinella brachycarpa</i> transcription activator. homeobox-leucine zipper protein.
BAA93463.1	AB028075	<i>Physcomitrella patens</i> homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
CAA06728.1	AJ005833	<i>Craterostigma plantagineum</i> transcription factor. homeodomain leucine zipper protein. hb-2.

AAD37695.1	AF145726	Oryza sativa homeodomain leucine zipper protein. Oshox2. transcription factor.
CAA65456.2	X96681	Oryza sativa transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.
AAF19980.1	AF211193	Oryza sativa homeodomain-leucine zipper transcription factor. Hox1. hox1.
AAK31270.1	AC079890	Oryza sativa homeodomain leucine zipper protein hox1. OSJNBb0089A17.12.
CAA63222.1	X92489	Glycine max transcription activator. homeobox-leucine zipper protein.
CAA06717.1	AJ005820	Craterostigma plantagineum transcription factor. homeodomain leucine zipper protein. hb-1.
AAA79778.1	L48485	Helianthus annuus homeodomain protein. putative.
SEQ ID NO: 831		
CAA06334.1	AJ005077	Lycopersicon esculentum protein kinase. TCTR2 protein. TCTR2.
AAG31141.1	AF305911	Oryza sativa EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAG31142.1	AF305912	Hordeum vulgare EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAK30005.1	AY029067	Rosa hybrid cultivar CTR2 protein kinase.
AAD46406.1	AF096250	Lycopersicon esculentum ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.
CAA73722.1	Y13273	Lycopersicon esculentum putative protein kinase.
AAD10057.1	AF110519	Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.
AAD10056.1	AF110518	Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.
AAA34002.1	M67449	Glycine max protein kinase. PK6.
AAK11734.1	AY027437	Arachis hypogaea serine/threonine/tyrosine kinase.
BAB16918.1	AP002863	Oryza sativa putative protein kinase. P0005A05.22.
CAC09580.1	AJ298992	Fagus sylvatica Abscisic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.

CAA97692.1	Z73295	Catharanthus roseus receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
AAF59906.1	AF197947	Glycine max receptor protein kinase-like protein. CLV1B.
AAF59905.1	AF197946	Glycine max receptor protein kinase-like protein. CLV1A.
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
BAA87852.1	AP000816	Oryza sativa Similar to putative Ser/Thr protein kinase. (AC004218).
BAB40094.1	AP003210	Oryza sativa putative receptor protein kinase. OSJNBa0010K01.7.
BAA92221.1	AP001278	Oryza sativa Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
CAA08995.1	AJ010091	Brassica napus MAP3K alpha 1 protein kinase. MAP3K alpha 1.
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
CAB51834.1	00069	Oryza sativa l1332.5. contains eukaryotic protein kinase domain PF.
CAA08997.1	AJ010093	Brassica napus MAP3K beta 1 protein kinase. MAP3K beta 1.
CAB54520.1	AJ238845	Brassica napus putative role in cell cycle control. MAP3K epsilon 1 protein kinase. MAP3Ke1.
AAF34436.1	AF172282	Oryza sativa similar to mitogen-activated protein kinases. DUPR11.32.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAG25966.1	AF302082	Nicotiana tabacum cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
BAA06538.1	D31737	Nicotiana tabacum protein-serine/threonine kinase.
AAF76189.1	AF271206	Rosa hybrid cultivar CTR1-like protein kinase. Raf-like protein kinase.
BAA84787.1	AP000559	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

BAA83373.1	AP000391	Oryza sativa
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).		
AAF66615.1	AF142596	Nicotiana tabacum
LRR receptor-like protein kinase.		
AAF91322.1	AF244888	Glycine max
receptor-like protein kinase 1. RLK1. GmRLK1.		
AAD21872.1	AF078082	Phaseolus vulgaris
receptor-like protein kinase homolog RK20-1.		
CAA61510.1	X89226	Oryza sativa
leucine-rich repeat/receptor protein kinase. lrk2.		
BAA87853.1	AP000816	Oryza sativa
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).		
AAF91323.1	AF244889	Glycine max
receptor-like protein kinase 2. RLK2. GmRLK2.		
AAF91324.1	AF244890	Glycine max
receptor-like protein kinase 3. RLK3. GmRLK3.		
AAF43394.1	AF230501	Oryza sativa subsp. japonica
serine/threonine protein kinase. YK1.		
AAK16409.1	AF320086	Zea mays
serine threonine kinase 1. stkl1. expressed in mature tassel.		
AAK21965.1	AY028699	Brassica napus
receptor protein kinase PERK1.		
BAB39437.1	AP003338	Oryza sativa
receptor-like kinase. OJ1212_B09.6.		
AAK11568.1	AF318492	Lycopersicon hirsutum
Pto-like protein kinase B. LhirPtoB.		

SEQ ID NO: 832

AAF35901.1	AF230332	Zinnia elegans
expansin 2.		
CAC19184.1	AJ291817	Cicer arietinum
expansin.		
AAG13982.1	AF297521	Prunus avium
expansin 1. Exp1. PruavExp1.		
BAB19676.1	AB029083	Prunus persica
expansin. PchExp1.		
AAC33529.1	U93167	Prunus armeniaca
expansin. PA-Exp1.		
AAC33530.1	AF038815	Prunus armeniaca
expansin. Exp2.		
AAD47901.1	AF085330	Pinus taeda
expansin.		

AAB37746.1	U30382	Cucumis sativus expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.
AAF21101.1	AF159563	Fragaria x ananassa expansin. Exp2. ripening regulated.
AAB40634.1	U64890	Pinus taeda expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAB40637.1	U64893	Pinus taeda expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAB40635.1	U64891	Pinus taeda expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
CAB43197.1	AJ239068	Lycopersicon esculentum cell wall loosening enzyme. expansin2. exp2.
AAB40636.1	U64892	Pinus taeda expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAC64201.1	AF096776	Lycopersicon esculentum expansin. LeEXP2.
AAD49956.1	AF167360	Rumex palustris expansin. EXP1.
AAC96081.1	AF049354	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.
AAC39512.1	AF043284	Gossypium hirsutum expansin. GhEXP1. contains N-terminal signal peptide.
AAB81662.1	U85246	Oryza sativa expansin. Os-EXP4.
AAG13983.1	AF297522	Prunus avium expansin 2. Exp2. PruavExp2.
AAF32409.1	AF230276	Triphysaria versicolor alpha-expansin 3.
AAG32921.1	AF184233	Lycopersicon esculentum expansin. Exp10.

BAB32732.1	AB049406	<i>Eustoma grandiflorum</i> <u>expansin. Eg Expansin.</u>
AAF32411.1	AF230278	<i>Triphysaria versicolor</i> <u>alpha-expansin 1.</u>
AAF35902.1	AF230333	<i>Zinnia elegans</i> <u>expansin 3.</u>
AAB38074.1	U30477	<i>Oryza sativa</i> induces extension (creep) in plant cell walls. <u>expansin Os-EXP2. Os-EXP2.</u> former gene name RiExB.
AAC96080.1	AF049353	<i>Nicotiana tabacum</i> involved in acid-growth response. <u>alpha-expansin precursor. Nt-EXP4.</u> cell wall protein.
AAF17570.1	AF202119	<i>Marsilea quadrifolia</i> <u>alpha-expansin. EXP1. Mq-EXP1.</u>
CAC06433.1	AJ276007	<i>Festuca pratensis</i> <u>expansin. exp2.</u>
AAD13633.1	AF059489	<i>Lycopersicon esculentum</i> <u>expansin precursor. Exp5.</u>
CAC19183.1	AJ291816	<i>Cicer arietinum</i> <u>expansin.</u>
AAF62181.1	AF247163	<i>Oryza sativa</i> <u>alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.</u>
AAF62180.1	AF247162	<i>Oryza sativa</i> <u>alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.</u>
CAB46492.1	AJ243340	<i>Lycopersicon esculentum</i> <u>expansin9. exp9.</u>
BAA88200.1	AP000837	<i>Oryza sativa</i> EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAF32410.1	AF230277	<i>Triphysaria versicolor</i> <u>alpha-expansin 2.</u>
AAB37749.1	U30460	<i>Cucumis sativus</i> <u>expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.</u>
CAA04385.1	AJ000885	<i>Brassica napus</i> Cell wall extension in plants. <u>Expansin.</u>
AAF17571.1	AF202120	<i>Regnellidium diphyllum</i> <u>alpha-expansin. EXP1. Rd-EXP1.</u>
AAD13632.1	AF059488	<i>Lycopersicon esculentum</i> <u>expansin precursor. Exp4.</u>
CAA06271.2	AJ004997	<i>Lycopersicon esculentum</i> <u>expansin18. exp18.</u>

AAC63088.1	U82123	<i>Lycopersicon esculentum</i> expansin. LeEXP1. fruit ripening regulated expansin.
AAC96077.1	AF049350	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
AAF62182.1	AF247164	<i>Oryza sativa</i> alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.
CAC18802.1	AJ289154	<i>Glycine max</i> expansion of cell walls. expansin. dd2/63.
AAC96078.1	AF049351	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
AAG01875.1	AF291659	<i>Striga asiatica</i> alpha-expansin 3. Exp3.
CAA69105.1	Y07782	<i>Oryza sativa</i> expansin. RiExA.
AAC96079.1	AF049352	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
SEQ ID NO: 833		
AAA34030.1	J03492	<i>Spinacia oleracea</i> glycolate oxidase (EC 1.1.3.15).
AAB40396.1	U80071	<i>Mesembryanthemum crystallinum</i> glycolate oxidase. GOX.
BAA03131.1	D14044	<i>Cucurbita sp.</i> glycolate oxidase.
AAB82143.1	AF022740	<i>Oryza sativa</i> glycolate oxidase. GOX.
CAA63482.1	X92888	<i>Lycopersicon esculentum</i> conversion of glycolate to glyoxylate + H ₂ O ₂ . glycolate oxidase.
AAC32392.1	AF082874	<i>Medicago sativa</i> glycolate oxidase.
AAC33509.1	U62485	<i>Nicotiana tabacum</i> photorespiration. glycolate oxidase. GLO.
AAF03097.1	AF162196	<i>Lactuca sativa</i> glycolate oxidase.
SEQ ID NO: 838		
CAA06770.1	AJ005928	<i>Brassica napus</i> squalene epoxidase homologue. Sqp1;2.
CAA06773.1	AJ005931	<i>Brassica napus</i> squalene epoxidase homologue. Sqp1;1.
BAA24448.1	AB003516	<i>Panax ginseng</i> squalene epoxidase.
CAA06223.1	AJ004923	<i>Lycopersicon esculentum</i> Squalene epoxidase. ERG.

SEQ ID NO: 840

BAB12686.1 AP002746 *Oryza sativa*putative pyrophosphate-dependent phosphofructo-1-kinase. P0671B11.1. contains ESTs AU068014(C11507),C28532(C61484),AU090544(C61415).

BAA99438.1 AP002743 *Oryza sativa*putative pyrophosphate-dependent phosphofructo-1-kinase. P0710E05.25. contains ESTs AU068014(C11507),C28532(C61484),AU090544(C61415).

AAB88875.1 U93272 *Prunus armeniaca*pyrophosphate-dependent phosphofructo-1-kinase.

CAA83683.1 Z32850 *Ricinus communis*pyrophosphate-dependent phosphofructokinase beta subunit.

AAC67587.1 AF095521 *Citrus x paradisi*pyrophosphate-dependent phosphofructokinase alpha subunit. PPi-PFKa.

AAA63452.1 M55191 *Solanum tuberosum*pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta-subunit.

AAC67586.1 AF095520 *Citrus x paradisi*pyrophosphate-dependent phosphofructokinase beta subunit. PPi-PFKb. PFP.

AAA63451.1 M55190 *Solanum tuberosum*pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha-subunit.

CAA83682.1 Z32849 *Ricinus communis*pyrophosphate-dependent phosphofructokinase alpha subunit.

SEQ ID NO: 841

AAG60182.1 AC084763 *Oryza sativa*putative ethylene-responsive element binding protein. OSJNBa0027P10.12.

AAK31279.1 AC079890 *Oryza sativa*putative ethylene-responsive element binding protein. OSJNBb0089A17.16.

AAG43545.1 AF211527 *Nicotiana tabacum*Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*AP2-related transcription factor. CDBP. stress induced transcription factor.

BAA07321.1 D38123 *Nicotiana tabacum*ERF1. ethylene-responsive transcription factor.

BAA97122.1 AB016264 *Nicotiana sylvestris*ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

CAB93940.1 AJ238740 *Catharanthus roseus*putative transcription factor. AP2-domain DNA-binding protein. orca2.

BAA87068.1 AB035270 *Matricaria chamomilla*ethylene-responsive element binding protein1 homolog. McEREBP1.

BAA97124.1 AB016266 *Nicotiana sylvestris*ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

CAB96900.1	AJ251250	Catharanthus roseus transcription factor. AP2-domain DNA-binding protein. orca3.
CAB96899.1	AJ251249	Catharanthus roseus transcription factor. AP2-domain DNA-binding protein. orca3.
AAC62619.1	AF057373	Nicotiana tabacum transcription factor. ethylene response element binding protein 1. EREBP1.
BAA97123.1	AB016265	Nicotiana sylvestris ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
AAC24587.1	AF071893	Prunus armeniaca AP2 domain containing protein. AP2DCP.
CAC12822.1	AJ299252	Nicotiana tabacum AP2 domain-containing transcription factor. ap2.
AAF76898.1	AF274033	Atriplex hortensis apetala2 domain-containing protein.
BAA94514.2	AP001800	Oryza sativa Similar to Arabidopsis thaliana chromosome 4, BAC clone F9D16; putative Ap2 domain protein (AL035394).
AAC14323.1	AF058827	Nicotiana tabacum TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pt16.
AAD00708.1	U91857	Stylosanthes hamata ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
BAA76734.1	AB024575	Nicotiana tabacum ethylene responsive element binding factor.
BAB03248.1	AB037183	Oryza sativa ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
BAB16083.1	AB036883	Oryza sativa transcriptional repressor. osERF3. osERF3. ERF protein family ERF3 associated repression domain.
AAF23899.1	AF193803	Oryza sativa transcription factor EREBP1. EREBP/AP2-like transcription factor.
AAF05606.1	AF190770	Oryza sativa EREBP-like protein. tsh1. TSH1; induced by ethylene.
CAB93939.1	AJ238739	Catharanthus roseus putative transcription factor. AP2-domain DNA-binding protein. orca1.
BAA78738.1	AB023482	Oryza sativa EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to Arabidopsis thaliana AP2 domain containing protein RAP2.10 mRNA, partial cds.(AF003103).
AAG43548.1	AF211530	Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.

AAG43549.1 AF211531 *Nicotiana tabacum*
Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.

BAA99376.1 AP002526 *Oryza sativa*
ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370) correspond to a region
of the predicted gene. Similar to *Arabidopsis thaliana* BAC F21J9; AP2 domain protein.
(AC000103).

AAK31271.1 AC079890 *Oryza sativa*
putative transcriptional factor. OSJNBb0089A17.22.

AAK01089.1 AF298231 *Hordeum vulgare*
CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.

AAG59618.1 AF239616 *Hordeum vulgare*
CRT/DRE-binding factor. CBF.

AAC49567.1 U41466 *Zea mays*
Glossy15. Glossy15. AP2 DNA-binding domain protein; similar to the *Arabidopsis* floral
homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic
regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.

SEQ ID NO: 842

AAC32034.1 AF023472 *Hordeum vulgare*
peptide transporter. ptr1. PTR1; integral membrane protein.

BAB40113.1 AP003311 *Oryza sativa*
putative peptide transport protein. P0024G09.4. contains ESTs
D40448(S2437),C71800(E0368),AU102190(E2393),
AU055921(S20154),AU102191(E2393),AU055922(S20154),
C98524(E0368),AU097146(S2437).

BAB16458.1 AP002483 *Oryza sativa*
putative peptide transport protein. P0019D06.16. contains ESTs
D40448(S2437),C71800(E0368),AU102190(E2393),
AU055921(S20154),AU102191(E2393),AU055922(S20154),
C98524(E0368),AU097146(S2437).

AAD01600.1 AF016713 *Lycopersicon esculentum*
LeOPT1. LeOPT1. oligopeptide transporter.

AAF07875.1 AF140606 *Oryza sativa*
nitrate transporter. NRT1.

AAF20002.1 AF213936 *Prunus dulcis*
amino acid/peptide transporter. PTR2. similar to transporters of nitrogenous compounds.

AAG46153.1 AC018727 *Oryza sativa*
putative peptide transporter. OSJNBa0056G17.8.

CAC00544.1 AJ277084 *Nicotiana plumbaginifolia*
ion transport. putative low-affinity nitrate transporter. nrt1.1.

CAC00545.1 AJ277085 *Nicotiana plumbaginifolia*
ion transport. putative low-affinity nitrate transporter. nrt1.2.

AAA80582.1 U17987 *Brassica napus*
putative nitrate transporter. RCH2 protein.

CAC07206.1 AJ278966 *Brassica napus*
Low-affinity nitrate transporter. nitrate transporter. nrt1.

AAG21898.1 AC026815 *Oryza sativa*
putative peptide transport protein. OSJNBa0079L16.13.

BAB19758.1 AB052786 *Glycine max*
putative nitrate transporter NRT1-3. NRT1-3.

AAK15441.1 AC037426 *Oryza sativa*
putative nitrate transporter. OSJNBb0014I11.9.

AAG21906.1 AC026815 *Oryza sativa*
putative peptide transport protein. OSJNBa0079L16.9.

BAB19760.1 AB052788 *Glycine max*
nitrate transporter NRT1-5. NRT1-5.

AAG46154.1 AC018727 *Oryza sativa*
putative peptide transporter. OSJNBa0056G17.27.

BAB19757.1 AB052785 *Glycine max*
nitrate transporter NRT1-2. NRT1-2.

BAB19756.1 AB052784 *Glycine max*
nitrate transporter NRT1-1. NRT1-1.

BAB16322.1 AP002818 *Oryza sativa*
putative peptide transporter-like protein. P0436E04.4.

AAB69642.1 AF000392 *Lotus japonicus*
peptide transporter. LjNOD65.

CAA93316.1 Z69370 *Cucumis sativus*
nitrite transporter. NiTR1.

AAD16016.1 AF080545 *Nepenthes alata*
peptide transporter. PTR1.

BAB19759.1 AB052787 *Glycine max*
putative nitrate transporter NRT1-4. NRT1-4.

AAD42860.1 AF154930 *Prunus dulcis*
transporter-like protein. TLP1.

SEQ ID NO: 847

CAA61980.1 X89890 *Bidens pilosa*
Calmodulin.

AAF73157.1 AF150059 *Brassica napus*
calmodulin. CaM1. involved in seed germination.

BAA87825.1 AP000815 *Oryza sativa*
ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene.
Similar to O.sativa gene encoding calmodulin. (Z12828).

CAA67054.1 X98404 *Capsicum annuum*
calmodulin-2.

AAA87347.1 M88307 *Brassica juncea*
calmodulin.

AAA33397.1	L18912	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin. putative.
AAG27432.1	AF295637	<i>Elaeis guineensis</i> calmodulin.
CAA42423.1	X59751	<i>Daucus carota</i> calmodulin. Ccam-1.
AAG11418.1	AF292108	<i>Prunus avium</i> calmodulin.
AAA92681.1	U13882	<i>Pisum sativum</i> calcium-binding protein. calmodulin.
AAB46588.1	U83402	<i>Capsicum annuum</i> calmodulin.
AAA33706.1	M80836	<i>Petunia x hybrida</i> calmodulin. CAM81.
AAF65511.1	AF108889	<i>Capsicum annuum</i> calmodulin.
CAA43143.1	X60738	<i>Malus x domestica</i> Calmodulin. CaM.
AAA19571.1	U10150	<i>Brassica napus</i> calcium binding. calmodulin. bcm1.
CAA78301.1	Z12839	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin.
BAA88540.1	AP000969	<i>Oryza sativa</i> ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).
AAB36130.1	S81594	<i>Vigna radiata</i> auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.
AAC36059.1	AF042840	<i>Oryza sativa</i> calmodulin. CaM1.
AAA33901.1	L18913	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin. putative.
AAA33900.1	L18914	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin.
AAA34237.1	L20691	<i>Vigna radiata</i> calmodulin.
CAA78288.1	Z12828	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin.
AAA32938.1	M27303	<i>Hordeum vulgare</i> calmodulin.
CAA78287.1	Z12827	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin.

AAC49587.1	U49105	Triticum aestivum calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum calmodulin TaCaM3-3. calcium-binding protein.
AAC49583.1	U48692	Triticum aestivum calmodulin TaCaM2-3. calcium-binding protein.
AAC49585.1	U49103	Triticum aestivum calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum calmodulin TaCaM3-1. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum calmodulin TaCaM2-2. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	Triticum aestivum calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	Triticum aestivum calmodulin TaCaM1-1. calcium-binding.
AAA03580.1	L01431	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-2. putative.
AAC36058.1	AF042839	Oryza sativa calmodulin. CaM2.
AAA85156.1	U20296	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34014.1	L01432	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAD10244.1	AF030032	Phaseolus vulgaris calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
CAA36644.1	X52398	Medicago sativa calmodulin (AA 1-149).
AAA85155.1	U20294	Solanum tuberosum calcium-binding protein. calmodulin.
AAB68399.1	U79736	Helianthus annuus calmodulin. HaCaM.
AAA62351.1	U20295	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34238.1	L20507	Vigna radiata calmodulin.
AAA85157.1	U20297	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34013.1	L01430	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-1. putative.

AAA33705.1	M80831	Petunia x hybrida calmodulin-related protein. CAM53.
CAA74307.1	Y13974	Zea mays calmodulin.
CAA54583.1	X77397	Zea mays calmodulin. CaM2.
SEQ ID NO: 848		
CAA06486.1	AJ005340	Linum usitatissimum IAA amidohydrolase. homolog.
SEQ ID NO: 850		
BAB17350.1	AP002747	Oryza sativa putative nodulin. P0698G03.34. contains ESTs D39891(S1543),D41717(S4395),AU033037(S1543).
BAA85440.1	AP000616	Oryza sativa ESTs AU055729(S20023),AU055730(S20023) correspond to a region of the predicted gene.; similar to Medicago nodulin N21-like protein (AC004218).
CAB53493.1	AJ245900	Oryza sativa
CAA303720.1	protein. q3037.20.	Similar to Medicago nodulin N21 (MtN21).
SEQ ID NO: 852		
AAD16018.1	AF081514	Taxus canadensis prenyltransferase. geranylgeranyl diphosphate synthase. geranylgeranyl pyrophosphate synthase.
SEQ ID NO: 853		
BAB32588.1	AB055807	Momordica charantia inhibitor against trypsin. bgit.
AAA34180.1	J05094	Lycopersicon peruvianum proteinase inhibitor I precursor.
AAA34198.1	M59427	Lycopersicon peruvianum proteinase inhibitor I. proteinase inhibitor I.
CAB61327.1	AJ132473	Amaranthus hypochondriacus Proteinase inhibition. trypsin inhibitor.
AAA60745.1	J04099	Lycopersicon esculentum proteinase inhibitor I. ER1.
CAA78269.1	Z12623	Nicotiana tabacum Putative precursor of serine proteinase inhibitor type I. Pre-pro-proteinase inhibitor I.
CAA47461.1	X67076	Nicotiana tabacum inhibitor of microbial serine proteinases (major isoform). TIMPa.
CAA78265.1	Z12619	Nicotiana tabacum precursor for serine proteinase inhibitor I. Pre-pro-proteinase inhibitor I.
CAA47460.1	X67075	Nicotiana tabacum inhibitor of microbial serine proteinases (minor isoform). TIMPb.
AAA34067.1	M74102	Nicotiana sylvestris pre-pro-proteinase inhibitor I.

AAC49603.1 U30861 Solanum tuberosum
serine proteinase inhibitor. wound-inducible proteinase inhibitor I.

BAA02823.1 D13662 Nicotiana glauca X Nicotiana langsdorffii
genetic tumor-related proteinase inhibitor I precursor. GTI.

AAA34199.1 K03290 Lycopersicon esculentum
wound-induced proteinase inhibitor I prepropeptide.

AAA34200.1 M13938 Lycopersicon esculentum
proteinase inhibitor I. PIIF.

AAA69780.1 L06137 Solanum tuberosum
proteinase inhibitor I. pin1. putative.

AAA72133.1 L06985 Solanum tuberosum
proteinase inhibitor I. pin1. The 'a' of the first atg is missing.

CAA78259.1 Z12611 Solanum tuberosum
proteinase inhibitor I.

AAA69781.1 L06606 Solanum tuberosum
proteinase inhibitor I. precursor.

CAA48136.1 X67950 Solanum tuberosum
protease inhibitor I. pin1.

CAA47907.1 X67675 Solanum tuberosum
proteinase inhibitor I. pin1.

CAB71340.1 AJ250663 Hordeum vulgare
putative proteinase inhibitor. bci-7. similarity to subtilisin/chymotrypsin inhibitor.

CAA57677.1 X82187 Zea mays
serine proteinase inhibitor. substilin /chymotrypsin-like inhibitor. pis7.

CAA55588.1 X78988 Zea mays
proteinase inhibitor. MPI.

CAA49593.1 X69972 Zea mays
proteinase inhibitor. MPI.

AAA33816.1 M17108 Solanum tuberosum
proteinase inhibitor I. precursor.

CAA57307.1 X81647 Cucurbita maxima
Pumpkin fruit trypsin inhibitor. pfiAF4.

CAA57203.1 X81447 Cucurbita maxima
Pumpkin Fruit Chymotrypsin Inhibitor. pfiBM7.

SEQ ID NO: 859

AAC34855.1 AF082030 Hemerocallis hybrid cultivar
senescence-associated protein 5. SA5. mRNA accumulates in senescent petals and
accumulation is induced by exogenous ABA.

AAG13616.1 AC078840 Oryza sativa
putative senescence-associated protein. OSJNBb0073N24.21.

SEQ ID NO: 864

AAF62403.1 AF212183 Nicotiana tabacum
harpin inducing protein. hin1. similar to hin1 protein.

CAA68848.1 Y07563 Nicotiana tabacum
activated during hypersensitive response. hin1.

AAB97367.1 AF039532 Oryza sativa
harpin induced gene 1 homolog. Hin1.

SEQ ID NO: 871

AAC61839.1 AF025430 Papaver somniferum
berberine bridge enzyme. bbe1. (S)-reticuline:oxygen oxidoreductase (methylene bridge forming).

AAB20352.1 S65550 Eschscholzia californica
(S)-reticuline:oxygen oxidoreductase (methylene-bridge-forming). /gene="(S)-reticuline:oxygen oxidoreductase. This sequence comes from Fig 2; berberine bridge enzyme.

AAC39358.1 AF005655 Eschscholzia californica
oxidizes the N-methyl group of (S)-reticuline to the berberine bridge carbon C-8 of (S)-scoulerine in berberine and benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbe1. covalently-bound FAD-dependent oxidase; elicitor-inducible.

AAD17487.1 AF049347 Berberis stolonifera
Catalyzes the oxidative cyclization of the N-methyl group of (S)-reticuline into the berberine bridge carbon (C-8) of (S)-scoulerine. berberine bridge enzyme. bbe1. Covalently flavylylated oxidase of isoquinoline alkaloid biosynthesis in plants.

SEQ ID NO: 872

AAF98369.1 AF158253 Nicotiana tabacum
patatin-like protein 3. PAT3. NtPat3.

CAA73328.1 Y12793 Cucumis sativus
mobilization of fat during seed germination. patatin-like protein.

CAA11042.1 AJ223039 Hevea brasiliensis
latex allergen. sequence similarity to patatins.

AAF25553.1 AF113546 Hevea brasiliensis
latex protein allergen Hev b 7. putative PLA2; similar to Solanum tubulin patatin encoded by GenBank Accession Number X03932.

CAA11041.1 AJ223038 Hevea brasiliensis
latex allergen. with sequence similarity to patatins.

AAC27724.1 U80598 Hevea brasiliensis
latex patatin homolog. putative PLA2; latex protein allergen; similar to Solanum tubulin patatin encoded by GenBank Accession Number X03932.

AAK27797.1 AF318315 Vigna unguiculata
patatin-like protein.

AAK18751.1 AF193067 Vigna unguiculata
patatin-like protein.

AAB08428.1 U68484 Nicotiana tabacum
patatin homolog.

AAD22170.1 AF061282 Sorghum bicolor
patatin-like protein.

AAF98368.1 AF158027	Nicotiana tabacum patatin-like protein 1. PAT1. NtPat1.
AAD22169.1 AF061282	Sorghum bicolor patatin-like protein.
CAA81735.1 Z27221	Solanum tuberosum patatin.
CAA31575.1 X13178	Solanum tuberosum patatin B2 (AA 1 - 386).
AAA33819.1 M18880	Solanum tuberosum patatin.
CAA31576.1 X13179	Solanum tuberosum patatin B1 (377 AA) (1 is 3rd base in codon).
CAA27588.1 X03956	Solanum tuberosum patatin.
AAA33828.1 M21879	Solanum tuberosum patatin.
CAA27571.1 X03932	Solanum tuberosum patatin.
CAA25592.1 X01125	Solanum tuberosum patatin.
AAA66198.1 U09331	Solanum brevidens patatin precursor.
AAB08427.1 U68483	Nicotiana tabacum patatin homolog.
AAF98370.1 AF158254	Nicotiana tabacum patatin-like protein 2. PAT2.
AAD22149.1 AF061282	Sorghum bicolor patatin-like protein. similar to the EST sequences E0496(panicle at flowering stage), R2382 (root), R2382 (root), S4036 (shoot), S3728 (shoot), S13457 (green shoot).
SEQ ID NO: 875	
BAA93022.1 AP001552	Oryza sativa ESTs C74776(E51022),C26123(C116681) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana cultivar Landsberg extra-large G-protein (AF060942).
SEQ ID NO: 876	
BAA87853.1 AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
AAK21965.1 AY028699	Brassica napus receptor protein kinase PERK1.
AAD21872.1 AF078082	Phaseolus vulgaris receptor-like protein kinase homolog RK20-1.
AAK00425.1 AC069324	Oryza sativa Putative protein kinase. OSJNBA0071K19.11.

BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAA33915.1	L27821	Oryza sativa receptor type serine/threonine kinase. protein kinase.
BAA82556.1	AB030083	Populus nigra lectin-like protein kinase. PnLPK.
AAK11674.1	AF339747	Lophopyrum elongatum protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAG59657.1	AC084319	Oryza sativa putative protein kinase. OSJNBA0004B24.20.
AAG03090.1	AC073405	Oryza sativa Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAB93834.1	U82481	Zea mays KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAF66615.1	AF142596	Nicotiana tabacum LRR receptor-like protein kinase.
AAG25966.1	AF302082	Nicotiana tabacum cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
AAB09771.1	U67422	Zea mays CRINKLY4 precursor. cr4. receptor kinase homolog.
AAF34428.1	AF172282	Oryza sativa receptor-like protein kinase. DUPR11.18.
BAB07906.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.14.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
BAA94516.1	AP001800	Oryza sativa Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA87852.1	AP000816	Oryza sativa Similar to putative Ser/Thr protein kinase. (AC004218).
BAA92221.1	AP001278	Oryza sativa Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
CAA73134.1	Y12531	Brassica oleracea serine/threonine kinase. BRLK.
BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).

AAG16628.1	AY007545	Brassica napus protein serine/threonine kinase BNK1.
CAB51834.1	00069	Oryza sativa l1332.5. contains eukaryotic protein kinase domain PF.
BAA06538.1	D31737	Nicotiana tabacum protein-serine/threonine kinase.
CAA73133.1	Y12530	Brassica oleracea serine /threonine kinase. ARLK.
CAB89179.1	AJ245479	Brassica napus subsp. napus ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus serine/threonine kinase receptor.
BAA92837.1	AB032474	Brassica oleracea S60 S-locus receptor kinase. SRK60.
AAA33000.1	M76647	Brassica oleracea receptor protein kinase. SKR6.
CAA79355.1	Z18921	Brassica oleracea S-receptor kinase-like protein.
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
CAA74661.1	Y14285	Brassica oleracea SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAA62232.1	U00443	Brassica napus S-receptor kinase. protein contains an immunoglobulin-like domain.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
BAB07904.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.12.
BAA94518.1	AP001800	Oryza sativa Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAA07577.2	D38564	Brassica rapa receptor protein kinase SRK12.
CAA74662.1	Y14286	Brassica oleracea SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAA07576.1	D38563	Brassica rapa receptor protein kinase SRK8.
BAB07999.1	AP002525	Oryza sativa putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB07905.1	AP002835	Oryza sativa putative S-receptor kinase. P0417G05.13.

BAB03429.1 AP002817 Oryza sativa
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

SEQ ID NO: 883

BAA90510.2 AP001111 Oryza sativa
rice EST AU030811, similar to rice Ca²⁺-ATPase (U82966).

AAF73985.1 AF096871 Zea mays
calcium pump. calcium ATPase. cap1.

CAA63790.1 X93592 Dunaliella bioculata
P-type ATPase. ca1. calcium pumping; CA1.

AAD11618.1 AF050496 Lycopersicon esculentum
Ca²⁺-ATPase. LCA1B; alternative transcript.

AAA34138.1 M96324 Lycopersicon esculentum
The calcium ATPase is a calcium ion pump. Ca²⁺-ATPase. LCA1.

AAB58910.1 U82966 Oryza sativa
Ca²⁺-ATPase.

AAD11617.1 AF050495 Lycopersicon esculentum
Ca²⁺-ATPase. LCA1A; alternative transcript.

AAG28435.1 AF195028 Glycine max
plasma membrane Ca²⁺-ATPase. SCA1.

AAG28436.1 AF195029 Glycine max
plasma membrane Ca²⁺-ATPase. SCA2.

CAA68234.1 X99972 Brassica oleracea
calmodulin-stimulated calcium-ATPase.

AAD31896.1 AF145478 Mesembryanthemum crystallinum
calcium ATPase.

AAB60276.1 U09989 Zea mays
H(+) -transporting ATPase. Mha1.

CAB69824.1 AJ271439 Prunus persica
plasma membrane H⁺ ATPase. PPA1.

AAD46187.1 AF156683 Nicotiana plumbaginifolia
plasma membrane proton ATPase. pma8.

BAA01058.1 D10207 Oryza sativa
H-ATPase. OSA1.

AAB49042.1 U54690 Dunaliella acidophila
plasma membrane proton ATPase. dha1. DaDHA1; proton pump.

AAA34173.1 M60166 Lycopersicon esculentum
H⁺-ATPase. LHA1.

CAA52107.1 X73901 Dunaliella bioculata
plasma membrane ATPase. pmal.

AAB35314.2 S79323 *Vicia faba*

plasma membrane H(+) -ATPase precursor. plasma membrane H(+) -ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.

BAA06629.1 D31843 *Oryza sativa*

plasma membrane H+-ATPase. OSA2.

AAA34094.1 M80489 *Nicotiana plumbaginifolia*

plasma membrane H+ ATPase. pma1.

BAA08134.1 D45189 *Zostera marina*

plasma membrane H+-ATPase. zha1.

CAB85494.1 AJ132891 *Medicago truncatula*

proton pump. H+-ATPase. ha1.

CAB85495.1 AJ132892 *Medicago truncatula*

proton pump. H+-ATPase. ha1.

AAB84202.2 AF029256 *Kosteletzky virginica*

plasma membrane proton ATPase. ATP1.

CAA47275.1 X66737 *Nicotiana plumbaginifolia*

plasma membrane H+-ATPase. pma4.

CAA54045.1 X76535 *Solanum tuberosum*

H(+) -transporting ATPase. PHA2.

AAD46186.1 AF156679 *Nicotiana plumbaginifolia*

plasma membrane proton ATPase. pma6.

AAB17186.1 U72148 *Lycopersicon esculentum*

plasma membrane H+-ATPase. LHA4. plasma membrane proton pumping ATPase.

CAB69823.1 AJ271438 *Prunus persica*

plasma membrane H+ ATPase. PPA2.

AAB41898.1 U84891 *Mesembryanthemum crystallinum*

plasma membrane proton pump. H+-transporting ATPase. PMA.

CAC29436.1 AJ310524 *Vicia faba*

P-type H+-ATPase. ha5. predominantly expressed in guard cells and flowers.

BAA37150.1 AB022442 *Vicia faba*

p-type H+-ATPase. VHA2.

CAA59800.1 X85805 *Zea mays*

H(+) -transporting ATPase. MHA-2.

CAA59799.1 X85804 *Phaseolus vulgaris*

H(+) -transporting ATPase. BHA-1.

CAC29435.1 AJ310523 *Vicia faba*

P-type H+-ATPase. vha4. predominantly expressed in flowers.

AAD46188.1 AF156691 *Nicotiana plumbaginifolia*

plasma membrane proton ATPase. pma9.

AAA34099.1 M80491 *Nicotiana plumbaginifolia*

plasma membrane H+ ATPase. pma3.

AAA34052.1	M27888	Nicotiana plumbaginifolia H ⁺ -translocating ATPase.
CAA54046.1	X76536	Solanum tuberosum H(+) -transporting ATPase. PHA1.
AAA34098.1	M80490	Nicotiana plumbaginifolia plasma membrane H ⁺ ATPase. pma3.
AAD55399.1	AF179442	Lycopersicon esculentum plasma membrane H ⁺ -ATPase isoform LHA2. LHA2.
AAF98344.1	AF275745	Lycopersicon esculentum plasma membrane H ⁺ -ATPase. LHA2. P-type ion pump.
AAG01028.1	AF289025	Cucumis sativus plasma membrane H ⁺ -ATPase.
AAK31799.1	AY029190	Lilium longiflorum plasma membrane H ⁺ ATPase. LILHA1.
AAA81348.1	U38965	Vicia faba p-type H ⁺ -ATPase. VHA2.
AAK32119.1	AF308817	Hordeum vulgare plasmalemma H ⁺ -ATPase 2.
AAK32118.1	AF308816	Hordeum vulgare plasmalemma H ⁺ -ATPase 1.
AAA20600.1	U08984	Zea mays plasma-membrane H ⁺ ATPase. Zmpma1.
SEQ ID NO: 884		
AAD21872.1	AF078082	Phaseolus vulgaris receptor-like protein kinase homolog RK20-1.
AAB93834.1	U82481	Zea mays KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA73134.1	Y12531	Brassica oleracea serine/threonine kinase. BRLK.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
CAA67145.1	X98520	Brassica oleracea receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea serine /threonine kinase. ARLK.
BAA23676.1	AB000970	Brassica rapa receptor kinase 1. BcRK1.
CAB41879.1	Y18260	Brassica oleracea SRK15 protein. SRK15. receptor-like kinase.
CAB41878.1	Y18259	Brassica oleracea SRK5 protein. SRK5. receptor-like kinase.

CAA74662.1	Y14286	Brassica oleracea
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.		
CAA74661.1	Y14285	Brassica oleracea
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.		
BAA06285.1	D30049	Brassica rapa
S-receptor kinase SRK9.		
BAA21132.1	D88193	Brassica rapa
S-receptor kinase. SRK9 (B.c.).		
BAA92836.1	AB032473	Brassica oleracea
S18 S-locus receptor kinase. SRK18.		
CAA79355.1	Z18921	Brassica oleracea
S-receptor kinase-like protein.		
AAA33000.1	M76647	Brassica oleracea
receptor protein kinase. SKR6.		
AAA62232.1	U00443	Brassica napus
S-receptor kinase. protein contains an immunoglobulin-like domain.		
AAA33008.1	M97667	Brassica napus
serine/threonine kinase receptor.		
CAB89179.1	AJ245479	Brassica napus subsp. napus
ser /thr kinase. S-locus receptor kinase. srk.		
BAB18292.1	AP002860	Oryza sativa
putative receptor-like protein kinase. P0409B08.19.		
AAD52097.1	AF088885	Nicotiana tabacum
receptor-like kinase CHRK1. Chrk1.		
BAA92837.1	AB032474	Brassica oleracea
S60 S-locus receptor kinase. SRK60.		
BAB21001.1	AB054061	Brassica rapa
S locus receptor kinase. SRK22.		
BAA07576.1	D38563	Brassica rapa
receptor protein kinase SRK8.		
BAA07577.2	D38564	Brassica rapa
receptor protein kinase SRK12.		
AAK02023.1	AC074283	Oryza sativa
Putative protein kinase-like. OSJNBa0087H07.5.		
CAA79324.1	Z18884	Brassica oleracea
S-receptor kinase related protein.		
BAB16871.1	AP002537	Oryza sativa
putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).		

BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
CAB51836.1	AJ243961	Oryza sativa Putitive Ser/Thr protein kinase. 11332.7.
AAA33915.1	L27821	Oryza sativa receptor type serine/threonine kinase. protein kinase.
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
AAF66615.1	AF142596	Nicotiana tabacum LRR receptor-like protein kinase.
BAB17139.1	AP002867	Oryza sativa putative receptor kinase. P0463F06.31.
SEQ ID NO: 885		
CAA80358.1	Z22645	Solanum tuberosum cleavage of sucrose to glucose and fructose. beta-fructofuranosidase.
CAA79676.1	Z21486	Solanum tuberosum cleavage of sucrose to glucose and fructose. beta-fructofuranosidase.
CAA57428.1	X81834	Nicotiana tabacum beta-fructofuranosidase. Ntbfruc1. beta-fructosidase.
CAA49162.1	X69321	Daucus carota beta-fructofuranosidase. Inval*DC1.
CAA57389.1	X81792	Chenopodium rubrum beta-fructofuranosidase. CIN1.
AAC17166.1	AF063246	Pisum sativum hydrolyzes sucrose to glucose and fructose. cell wall invertase. bfruct1. isoform Pcl-2; the Pcl-1 isoform is in the file with GenBank Accession Number X85327; beta-fructofuranosidase.
CAA59677.1	X85327	Pisum sativum hydrplyze sucrose into fructose and glucose. invertase. bfruct1. beta-fructofuranosidase.
AAD02263.1	AF043346	Zea mays sucrose hydrolysis. cell wall invertase. incw3. Incw3; beta-fructofuranosidase.
CAA84526.1	Z35162	Vicia faba hydrolyze sucrose. beta-fructofuranosidase; cell wall invertase I; fructosidase. VFCWINV1.

AAC96065.1 AF030420 *Triticum aestivum*
hydrolyzes sucrose. cell wall invertase. IVR1. hydrolase; beta-fructofuranosidase;
fructosidase.

CAA53099.1 X75353 *Daucus carota*
beta-fructofuranosidase.

AAB68679.1 U92438 *Phaseolus vulgaris*
soluble acid invertase. PVSAI; potential vacuolar targeted enzyme; beta-fructofuranosidase.

CAA89992.1 Z49831 *Vicia faba*
hydrolyze sucrose. vacuolar invertase; beta-fructofuranosidase. VFVCINV.

CAA53097.1 X75351 *Daucus carota*
beta-fructofuranosidase.

CAA77267.1 Y18707 *Daucus carota*
beta-fructofuranosidase, isoform I. Inv*Dc4. soluble acid invertase.

CAA53098.1 X75352 *Daucus carota*
beta-fructofuranosidase.

CAA77266.1 Y18706 *Daucus carota*
beta-fructofuranosidase, isoform II. Inv*Dc5. soluble acid invertase.

AAC96066.1 AF030421 *Triticum aestivum*
hydrolyzes sucrose. cell wall invertase. IVR3. hydrolase; beta-fructofuranosidase;
fructosidase.

AAG36943.1 AF274299 *Brassica oleracea*
cleaves sucrose into glucose and fructose at acid pH optima. acid invertase AI7-3. sucrose
hydrolysing enzyme; beta-fructofuranosidase.

SEQ ID NO: 887

AAD10836.1 U52079 *Solanum tuberosum*
P-glycoprotein. pmdr1. binds ATP; ATPase; transporter; transmembrane protein.

BAA96612.1 AP002482 *Oryza sativa*
Similar to *Arabidopsis thaliana* chromosome 2, BAC F14M4 ; putative ABC transporter
(AC004411).

AAG49002.1 AY013246 *Hordeum vulgare*
putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative
sequencing.

AAG45492.1 AY013245 *Oryza sativa*
36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and
comparative sequence.

BAA83352.1 AP000391 *Oryza sativa*
ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.;
Similar to ABC transporter-7 (U43892).

AAG49003.1 AY013246 *Hordeum vulgare*
putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and
comparative sequence.

BAB17113.1 AP002866 *Oryza sativa*
putative white protein; ATP-binding cassette transporter. P0410E01.34.

BAA90508.1 AP001111 Oryza sativa
similar to ABC transporter of Arabidopsis thaliana (AC004697).

BAA90507.1 AP001111 Oryza sativa
similar to ABC transporter of Arabidopsis thaliana (AC004697).

BAB16495.1 AP002861 Oryza sativa
putative ABC transporter ATP-binding protein. P0665D10.21.

BAB21276.1 AP002844 Oryza sativa
putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).

BAB21275.1 AP002844 Oryza sativa
putative ABC transporter protein. P0410E03.6.

BAB21273.1 AP002844 Oryza sativa
putative ABC transporter protein. P0410E03.4.

BAB40032.1 AP003046 Oryza sativa
putative ABC transporter. P0445D12.3.

SEQ ID NO: 888

AAD21872.1 AF078082 Phaseolus vulgaris
receptor-like protein kinase homolog RK20-1.

CAA73134.1 Y12531 Brassica oleracea
serine/threonine kinase. BRLK.

AAB93834.1 U82481 Zea mays
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

AAC23542.1 U20948 Ipomoea trifida
receptor protein kinase. IRK1.

AAA33000.1 M76647 Brassica oleracea
receptor protein kinase. SKR6.

CAB89179.1 AJ245479 Brassica napus subsp. napus
ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1 M97667 Brassica napus
serine/threonine kinase receptor.

CAA74661.1 Y14285 Brassica oleracea
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

CAA67145.1 X98520 Brassica oleracea
receptor-like kinase. SFR2.

AAA62232.1 U00443 Brassica napus
S-receptor kinase. protein contains an immunoglobulin-like domain.

CAA73133.1 Y12530 Brassica oleracea
serine /threonine kinase. ARLK.

BAA23676.1 AB000970 Brassica rapa
receptor kinase 1. BcRK1.

BAA92836.1 AB032473 Brassica oleracea
S18 S-locus receptor kinase. SRK18.

CAA74662.1	Y14286	Brassica oleracea
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.		
CAA79355.1	Z18921	Brassica oleracea
S-receptor kinase-like protein.		
CAB41879.1	Y18260	Brassica oleracea
SRK15 protein. SRK15. receptor-like kinase.		
BAA06285.1	D30049	Brassica rapa
S-receptor kinase SRK9.		
BAA21132.1	D88193	Brassica rapa
S-receptor kinase. SRK9 (B.c).		
CAB41878.1	Y18259	Brassica oleracea
SRK5 protein. SRK5. receptor-like kinase.		
BAA92837.1	AB032474	Brassica oleracea
S60 S-locus receptor kinase. SRK60.		
BAA07577.2	D38564	Brassica rapa
receptor protein kinase SRK12.		
BAB21001.1	AB054061	Brassica rapa
S locus receptor kinase. SRK22.		
BAA07576.1	D38563	Brassica rapa
receptor protein kinase SRK8.		
AAD52097.1	AF088885	Nicotiana tabacum
receptor-like kinase CHRK1. Chrk1.		
AAK02023.1	AC074283	Oryza sativa
Putative protein kinase-like. OSJNBa0087H07.5.		
BAB18292.1	AP002860	Oryza sativa
putative receptor-like protein kinase. P0409B08.19.		
BAA87853.1	AP000816	Oryza sativa
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).		
AAK21965.1	AY028699	Brassica napus
receptor protein kinase PERK1.		
BAB21240.1	AP002953	Oryza sativa
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).		
BAB39873.1	AP002882	Oryza sativa
putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).		
BAB17331.1	AP002747	Oryza sativa
putative receptor kinase. P0698G03.12.		
BAB17139.1	AP002867	Oryza sativa
putative receptor kinase. P0463F06.31.		
AAK00425.1	AC069324	Oryza sativa
Putative protein kinase. OSJNBa0071K19.11.		

BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
CAB51836.1	AJ243961	Oryza sativa Putitive Ser/Thr protein kinase. 11332.7.
AAF78016.1	AF238472	Oryza sativa receptor-like kinase. RLG15. protein kinase.
BAB39451.1	AP003338	Oryza sativa putative receptor kinase. OJ1212_B09.24.
SEQ ID NO: 890		
AAB47181.1	S82324	Zea mays /gene="calcium/calmodulin-dependent protein kinase. This sequence comes from Fig. 1.
BAA22410.1	D38452	Zea mays calcium-dependent protein kinase-related kinase.
BAA12692.1	D84508	Zea mays CDPK-related protein kinase. Does not require calcium for its activity.
AAG01179.1	AF289237	Zea mays calcium/calmodulin dependent protein kinase MCK2. MCK2.
CAA58750.1	X83869	Daucus carota CDPK-related protein kinase. CRK (or PK421).
BAA12691.1	D84507	Zea mays CDPK-related protein kinase. Does not require calcium for its activity (by similarity).
AAC24961.1	AF009337	Tradescantia virginiana CDPK-related protein kinase. CRK1.
AAF23901.2	AF194414	Oryza sativa calcium-dependent protein kinase. CDPK5. OsCDPK5.
AAF23900.1	AF194413	Oryza sativa calcium-dependent protein kinase. CDPK1. OsCDPK1.
AAC78558.1	AF030879	Solanum tuberosum protein kinase CPK1.
AAD17800.1	AF090835	Mesembryanthemum crystallinum Ca2+-dependent protein kinase. CPK1. serine/threonine protein kinase.
AAB49984.1	U90262	Cucurbita pepo calcium-dependent calmodulin-independent protein kinase CDPK. cpCPK1. serine/threonine protein kinase that is activated by direct binding of calcium.
CAA07481.1	AJ007366	Zea mays calcium-dependent protein kinase.
BAB21081.1	AP002819	Oryza sativa putative calcium-dependent protein kinase. P0501G01.10.
BAA12715.1	D85039	Zea mays calcium-dependent protein kinase.

AAC25423.1	AF072908	Nicotiana tabacum calcium-dependent protein kinase. CDPK1.
CAA39936.1	X56599	Daucus carota calcium- dependent protein kinase. DcPK431.
CAA57157.1	X81394	Oryza sativa calcium-dependent protein kinase. OSCPK2.
AAF21062.1	AF216527	Dunaliella tertiolecta calcium-dependent protein kinase. CPK1; CDPK.
BAA81751.1	AB017517	Marchantia polymorpha calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
BAA81749.1	AB017515	Marchantia polymorpha calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
AAB88537.1	AF035944	Fragaria x ananassa calcium-dependent protein kinase. MAX17.
BAA81750.1	AB017516	Marchantia polymorpha calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
BAA81748.1	AB017515	Marchantia polymorpha calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
AAA69507.1	U28376	Zea mays calcium-dependent protein kinase. MZECDPK2.
AAA61682.1	L27484	Zea mays calcium-dependent protein kinase. CDPK.
AAB80693.1	U69174	Glycine max calmodulin-like domain protein kinase isoenzyme gamma. CDPK gamma.
BAA13232.1	D87042	Zea mays Calcium-dependent protein kinase.
BAA13440.1	D87707	Ipomoea batatas calcium dependent protein kinase. CDPK.
CAA89202.1	Z49233	Chlamydomonas eugametos calcium-stimulated protein kinase.
AAB70706.1	U82087	Tortula ruralis calmodulin-like domain protein kinase. TrCPK1.
AAD28192.2	AF115406	Solanum tuberosum calcium-dependent protein kinase. CDPK; catalytic domain.
AAC49405.1	U08140	Vigna radiata calcium dependent protein kinase. CDPK.
BAA12338.1	D84408	Zea mays calcium dependent protein kinase. ZmCDPK1.
CAA65500.1	X96723	Medicago sativa protein kinase. CDPK.

BAA85396.1 AP000615 *Oryza sativa*
ESTs C22369(C12239),C22370(C12239), AU057852(S21844),AU057853(S21844)
correspond to a region of the predicted gene.; similar to calcium dependent protein kinase.
(AF048691).

AAA33443.1 L15390 *Zea mays*
calcium-dependent protein kinase. CDPK.

AAB80692.1 U69173 *Glycine max*
calmodulin-like domain protein kinase isoenzyme beta. CDPK beta.

CAA57156.1 X81393 *Oryza sativa*
calcium-dependent protein kinase. OSCPKII.

AAC05270.1 AF048691 *Oryza sativa*
calcium dependent protein kinase. CDPK12.

AAK26164.1 AY027885 *Cucumis sativus*
calcium-dependent calmodulin-independent protein kinase 5. CDPK5. CsCDPK5.

AAG46110.1 AC073166 *Oryza sativa*
calcium-dependent protein kinase. OSJNBb0064P21.2.

BAA02698.1 D13436 *Oryza sativa*
calcium-dependent protein kinase. spk.

BAA90814.1 AP001168 *Oryza sativa*
ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.;
Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).

AAF19401.1 AF203479 *Glycine max*
phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase
family; lacks the autoinhibitory region and EF hands.

CAB46228.1 Y18055 *Arachis hypogaea*
calcium dependent protein kinase. CDPK.

AAF19403.1 AF203481 *Lycopersicon esculentum*
phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase
family; lacks the autoinhibitory region and EF hands.

AAF19402.1 AF203480 *Lycopersicon esculentum*
phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca2+/CaM kinase
family; lacks the autoinhibitory region and EF hands.

SEQ ID NO: 892

AAF20931.1 AF206721 *Brassica juncea*
ascorbate oxidase.

BAA07734.1 D43624 *Nicotiana tabacum*
ascorbate oxidase precursor.

AAA33119.1 J04494 *Cucumis sativus*
ascorbate oxidase precursor (EC 1.10.3.3).

CAA75577.1 Y15295 *Medicago truncatula*
L-ascorbate oxidase. MtN23.

AAF35911.2 AF233594 *Cucumis melo*
ascorbate oxidase AO4. multicopper oxidase.

CAA39300.1	X55779	Cucurbita sp. ascorbate oxidase.
BAA09528.1	D55677	Cucurbita maxima ascorbate oxidase. AAO.
AAF35910.1	AF233593	Cucumis melo ascorbate oxidase AO1. multicopper oxidase.
CAA71275.1	Y10226	Cucumis melo L-ascorbate oxidase. ao3.
AAF20932.1	AF206722	Brassica juncea ascorbate oxidase.
AAF20933.1	AF206723	Brassica juncea ascorbate oxidase.
CAA71273.1	Y10224	Cucumis melo L-ascorbate oxidase. ao1.
CAA71274.1	Y10225	Cucumis melo L-ascorbate oxidase. ao1.
BAA20520.1	AB004799	Oryza sativa ascorbate oxidase.
AAF33751.1	AF202460	Capsicum annuum ascorbic acid oxidase.
AAB17193.1	U73105	Liriodendron tulipifera monolignol polymerization; lignin biosynthesis. laccase. LAC2-3. diphenol oxidase; blue copper oxidase.
AAB17191.1	U73103	Liriodendron tulipifera monolignol polymerization; lignin biosynthesis. laccase. LAC2-1. diphenol oxidase; blue copper oxidase.
AAC49536.1	U43542	Nicotiana tabacum diphenol oxidase. laccase.
AAB17194.1	U73106	Liriodendron tulipifera monolignol polymerization; lignin biosynthesis. laccase. LAC2-4. diphenol oxidase; blue copper oxidase.
AAB17192.1	U73104	Liriodendron tulipifera monolignol polymerization; lignin biosynthesis. laccase. LAC2-2. diphenol oxidase; blue copper oxidase.
AAC04576.1	AF047697	Oryza sativa p-diphenol oxidase. putative high-pI laccase.
AAB09228.1	U12757	Acer pseudoplatanus monolignol polymerization; lignin biosynthesis. laccase. diphenol oxidase.
CAA45554.1	X64257	Brassica napus Bp10. protein homologous to ascorbate oxidase.
AAC49538.1	U45243	Nicotiana tabacum diphenol oxidase. laccase.

AAC49537.1	U43543	Nicotiana tabacum diphenol oxidase. laccase.
AAD02557.1	AF049931	Petunia x hybrida PGPS/NH15. PGPS/NH15. ascorbate oxidase homolog.
SEQ ID NO: 894		
CAB43505.1	AJ239051	Cicer arietinum cytochrome P450. cyp81E2.
BAA74465.1	AB022732	Glycyrrhiza echinata cytochrome P450. CYP Ge-31.
BAA93634.1	AB025016	Lotus japonicus cytochrome P450.
BAA22422.1	AB001379	Glycyrrhiza echinata cytochrome P450. CYP81E1.
CAA04117.1	AJ000478	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'-race).
CAB41490.1	AJ238439	Cicer arietinum cytochrome P450 monooxygenase. cyp81E3v2.
CAA04116.1	AJ000477	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
CAA10067.1	AJ012581	Cicer arietinum cytochrome P450. cyp81E3.
AAK38079.1	AF321855	Lolium rigidum putative cytochrome P450.
AAK38080.1	AF321856	Lolium rigidum putative cytochrome P450.
AAK38081.1	AF321857	Lolium rigidum putative cytochrome P450.
AAD56282.1	AF155332	Petunia x hybrida flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAC34853.1	AF082028	Hemerocallis hybrid cultivar putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3. mRNA accumulates in senescing petals.
AAG09208.1	AF175278	Pisum sativum wound-inducible P450 hydroxylase. CYP82A1.
BAA12159.1	D83968	Glycine max Cytochrome P-450 (CYP93A1).
CAA71515.1	Y10491	Glycine max putative cytochrome P450.
CAA71876.1	Y10982	Glycine max putative cytochrome P450.
CAA65580.1	X96784	Nicotiana tabacum cytochrome P450. hsr515.

AAC49188.2	U29333	Pisum sativum cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
CAA71516.1	Y10492	Glycine max putative cytochrome P450.
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
AAC39454.1	AF014802	Eschscholzia californica (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to wound-inducible CYP82A1 of Pisum sativum GenBank Accession Number U29333.
AAB94590.1	AF022461	Glycine max CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
AAA32913.1	M32885	Persea americana cytochrome P-450LXXIA1 (cyp71A1).
CAA71877.1	Y10983	Glycine max putative cytochrome P450.
BAA84072.1	AB028152	Torenia hybrida flavone synthase II. cytochrome P450. TFNS5.
BAA13076.1	D86351	Glycine max cytochrome P-450 (CYP93A2).
AAG34695.1	AF313492	Matthiola incana putative cytochrome P450.
BAA84071.1	AB028151	Antirrhinum majus flavone synthase II. cytochrome P450. AFNS2.
AAC32274.1	AF081575	Petunia x hybrida flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.
BAA35080.1	AB015762	Nicotiana tabacum putative cytochrome P450. CYP82E1.
CAA50155.1	X70824	Solanum melongena flavonoid hydroxylase (P450). CYP75.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
BAA92894.1	AB006790	Petunia x hybrida cytochrome P450. IMT-2.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
AAB94587.1	AF022458	Glycine max CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

SEQ ID NO: 895

BAA78764.1 AB023482	Oryza sativa	
ESTs C98382(C2985),D22444(C11129)	correspond to a region of the predicted gene.; Similar to <i>Arabidopsis thaliana</i> APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).	
AAF43496.1 AF131222	Lophopyrum elongatum	
protein serine/threonine kinase. ESI47.	induced in roots by salt stress, osmotic stress, and ABA treatment.	
AAK11674.1 AF339747	Lophopyrum elongatum	
protein kinase. ESI47.		
AAG16628.1 AY007545	Brassica napus	
protein serine/threonine kinase BNK1.		
BAA94510.1 AB041504	Populus nigra	
protein kinase 2. PnPK2.		
BAA94509.1 AB041503	Populus nigra	
protein kinase 1. PnPK1.		
BAA87853.1 AP000816	Oryza sativa	
EST AU030604(E51294)	corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).	
BAB07999.1 AP002525	Oryza sativa	
putative protein kinase. P0462H08.22.	contains EST C22619(S11214).	
BAB03429.1 AP002817	Oryza sativa	
EST C22619(S11214)	corresponds to a region of the predicted gene. Similar to <i>Arabidopsis thaliana</i> chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).	
BAB16871.1 AP002537	Oryza sativa	
putative protein kinase APK1A <i>Arabidopsis thaliana</i> .	P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).	
BAB39873.1 AP002882	Oryza sativa	
putative protein kinase. P0439B06.8.	contains ESTs AU056701(S20808),AU056702(S20808).	
BAB39409.1 AP002901	Oryza sativa	
putative protein kinase. P0456F08.9.	contains EST C23560(R0290).	
AAK00425.1 AC069324	Oryza sativa	
Putative protein kinase. OSJNBa0071K19.11.		
BAB21240.1 AP002953	Oryza sativa	
Putative protein kinase. P0426D06.20.	contains ESTs C22359(C11461),C22360(C11461).	
AAK21965.1 AY028699	Brassica napus	
receptor protein kinase PERK1.		
AAG59657.1 AC084319	Oryza sativa	
putative protein kinase. OSJNBa0004B24.20.		
AAG03090.1 AC073405	Oryza sativa	
Similar to an <i>Arabidopsis</i> somatic embryogenesis receptor-like kinase (AC007504).		
CAB51834.1 00069	Oryza sativa	
l1332.5.	contains eukaryotic protein kinase domain PF.	

AAC61805.1	U28007	<i>Lycopersicon esculentum</i>
		serine/threonine protein kinase. Pto kinase interactor 1. Pt1. Pt1 kinase.
AAF91336.1	AF249317	<i>Glycine max</i>
		Pt1 kinase-like protein. Pt1a. protein kinase.
AAF91337.1	AF249318	<i>Glycine max</i>
		Pt1 kinase-like protein. Pt1b. protein kinase.
BAB21241.1	AP002953	<i>Oryza sativa</i>
		Putative Pto kinase interactor 1. P0426D06.21. contains ESTs
		AU108280(E0721),D48017(S13927).
AAB09771.1	U67422	<i>Zea mays</i>
		CRINKLY4 precursor. cr4. receptor kinase homolog.
CAA97692.1	Z73295	<i>Catharanthus roseus</i>
		receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
BAA92221.1	AP001278	<i>Oryza sativa</i>
		Similar to <i>Arabidopsis thaliana</i> chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	<i>Oryza sativa</i>
		Similar to putative Ser/Thr protein kinase. (AC004218).
AAB61708.1	U93048	<i>Daucus carota</i>
		somatic embryogenesis receptor-like kinase. SERK.
AAG25966.1	AF302082	<i>Nicotiana tabacum</i>
		cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
BAA90808.1	AP001168	<i>Oryza sativa</i>
		Similar to putative receptor-like protein kinase (AL035679).
AAF76313.1	AF220603	<i>Lycopersicon esculentum</i>
		Pto kinase. LescPth5.
AAB47421.1	U59316	<i>Lycopersicon esculentum</i>
		serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAC23542.1	U20948	<i>Ipomoea trifida</i>
		receptor protein kinase. IRK1.
BAB19337.1	AP003044	<i>Oryza sativa</i>
		putative protein kinase. P0038C05.10. contains ESTs
		AU056335(S20481),AU056336(S20481).
AAC27894.1	AF023164	<i>Zea mays</i>
		leucine-rich repeat transmembrane protein kinase 1. Itk1.
AAF66615.1	AF142596	<i>Nicotiana tabacum</i>
		LRR receptor-like protein kinase.
CAB51480.1	Y14600	<i>Sorghum bicolor</i>
		putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

BAA92954.1 AP001551	Oryza sativa
Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).	
BAA92953.1 AP001551	Oryza sativa
Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).	
AAK11566.1 AF318490	Lycopersicon hirsutum
Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.	
AAK11567.1 AF318491	Lycopersicon hirsutum
Pto-like protein kinase F. LhirPtoF.	
BAA82556.1 AB030083	Populus nigra
lectin-like protein kinase. PnLPK.	
CAA67145.1 X98520	Brassica oleracea
receptor-like kinase. SFR2.	

SEQ ID NO: 899

AAF61647.1 AF190634	Nicotiana tabacum
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.	
BAA89009.1 AB027455	Petunia x hybrida
anthocyanin 5-O-glucosyltransferase. PH1.	
AAA59054.1 L34847	Zea mays
conjugation of the growth hormone indole-3-acetic acid (IAA). IAA-glu synthetase. iaglu.	
BAA93039.1 AB033758	Citrus unshiu
limonoid UDP-glucosyltransferase. LGTase.	
BAA36423.1 AB013598	Verbena x hybrida
UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.	
BAA36421.1 AB013596	Perilla frutescens
UDP-glucose:anthocysnin 5-O-glucosyltransferase. PF3R4.	
AAF98390.1 AF287143	Brassica napus
catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.	
BAA36422.1 AB013597	Perilla frutescens
UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.	
BAB07962.1 AP002524	Oryza sativa
putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).	
AAK16175.1 AC079887	Oryza sativa
putative glucosyltransferase. OSJNBa0040E01.15.	
AAK16181.1 AC079887	Oryza sativa
putative glucosyltransferase. OSJNBa0040E01.16.	
AAK16178.1 AC079887	Oryza sativa
putative glucosyltransferase. OSJNBa0040E01.5.	
AAG25643.1 AF303396	Phaseolus vulgaris
UDP-glucosyltransferase HRA25. putative; defense associated.	

AAK16172.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.14.
BAA83484.1	AB031274	Scutellaria baicalensis UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAB36652.1	U32643	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum phenylpropanoid:glucosyltransferase 2. tog2. glucosyltransferase.
AAD21086.1	AF127218	Forsythia x intermedia adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
AAB36653.1	U32644	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS5a.
BAA12737.1	D85186	Gentiana triflora UDP-glucose:flavonoid-3-glucosyltransferase.
AAK28303.1	AF346431	Nicotiana tabacum phenylpropanoid:glucosyltransferase 1. tog1. glucosyltransferase.
AAF17077.1	AF199453	Sorghum bicolor UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
AAK16180.1	AC079887	Oryza sativa putative glucosyltransferase. OSJNBa0040E01.21.
CAA59450.1	X85138	Lycopersicon esculentum twi1. homologous to glucosyltransferases.
BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
BAB41026.1	AB047099	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
BAB41024.1	AB047097	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. AJUFGT2.
BAB41022.1	AB047095	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41020.1	AB047093	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAA89008.1	AB027454	Petunia x hybrida anthocyanidin 3-O-glucosyltransferase. PGT8.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.
CAB56231.1	Y18871	Dorotheanthus bellidiformis betanidin-5-O-glucosyltransferase.

AAB81683.1	AF000372	Vitis vinifera UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41019.1	AB047092	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41025.1	AB047098	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
BAB41023.1	AB047096	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
BAB41021.1	AB047094	Vitis vinifera UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
AAB81682.1	AF000371	Vitis vinifera UDP glucose:flavonoid 3-o-glucosyltransferase.
BAA19659.1	AB002818	Perilla frutescens flavonoid 3-O-glucosyltransferase. UDP glucose.
BAA90787.1	AB038248	Ipomoea batatas UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.
AAD04166.1	AF101972	Phaseolus lunatus catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
AAB86473.1	AF028237	Ipomoea purpurea UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
SEQ ID NO: 900		
AAA33975.1	M11395	Glycine max small heat shock protein.
CAA41547.1	X58711	Medicago sativa heat shock protein.
AAB03893.1	M11318	Glycine max 17.5 kd heat shock protein Gmhsp17.6L.
AAA33672.1	M33899	Pisum sativum 18.1 kDa heat shock protein (hsp18.1).
CAA25578.1	X01104	Glycine max heat shock protein 6871 (aa 1-153).
CAB55634.2	AJ237596	Helianthus annuus 17.9 kDa heat-shock protein. hsp17.9.
BAA33062.1	AB017273	Cuscuta japonica low-molecular-weight heat shock protein. CJHSP17.
AAA33974.1	M11317	Glycine max 17.6 kd heat shock protein Gmhsp17.6L.
AAD30454.1	AF123257	Lycopersicon esculentum 17.6 kD class I small heat shock protein. HSP17.6.
AAD30452.1	AF123255	Lycopersicon esculentum 17.7 kD class I small heat shock protein. HSP17.7.

CAA39603.1	X56138	Lycopersicon esculentum small heat shock protein (class I).
AAD30453.1	AF123256	Lycopersicon esculentum 17.8 kD class I small heat shock protein. HSP17.8.
CAA37847.1	X53851	Daucus carota heat shock protein.
AAA33671.1	M33900	Pisum sativum 17.9 kDa heat shock protein (hsp17.9).
AAF34133.1	AF161179	Malus x domestica low molecular weight heat shock protein. Hsp1.
CAA41546.1	X58710	Medicago sativa heat shock protein.
AAB63310.1	U46544	Helianthus annuus 18.6 kDa heat-shock protein. Class I low-molecular-weight heat-shock protein.
AAB63311.1	U46545	Helianthus annuus 17.7 kDa heat shock protein. Class I low-molecular-weight heat-shock protein.
CAB08441.1	Z95153	Helianthus annuus 17.6 kD class I small heat-shock protein HSP17.6. Ha hsp17.6.
CAA42222.1	X59701	Helianthus annuus 17.6 kDa heat shock protein.
AAC39360.1	U63631	Fragaria x ananassa LMW heat shock protein.
AAA33910.1	M80939	Oryza sativa 16.9 kDa heat shock protein.
CAA37848.1	X53852	Daucus carota heat shock protein.
AAA33909.1	M80938	Oryza sativa 16.9 kDa heat shock protein.
CAA43210.1	X60820	Oryza sativa 16.9 KD low molecular weight heat shock protein.
CAA37864.1	X53870	Chenopodium rubrum heat-shock protein.
AAD49336.1	AF166277	Nicotiana tabacum low molecular weight heat-shock protein. LHS-1. TLHS-1.
AAA61632.1	U08601	Papaver somniferum low molecular weight heat-shock protein.
AAB72109.1	AF022217	Brassica rapa low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.
CAA63902.1	X94192	Pennisetum glaucum heat shock protein 16.9. hsp16.9.
AAB39856.1	U81385	Oryza sativa heat shock protein. Oshsp16.9C. class I, low molecular mass.

CAA46641.1 X65725 Zea mays
 heat shock protein 17.2. Zmhsp 17.2. Class I low molecular weight heat shock protein.

CAA08908.1 AJ009880 Castanea sativa
 molecular chaperone. cytosolic class I small heat-shock protein HSP17.5. hsp17.5.

CAB93512.1 AJ243565 Brassica oleracea
 putative class I small heat shock protein. HSP17.7-a protein. hsp17.7-a.

CAA63903.1 X94193 Pennisetum glaucum
 heat shock protein 17.9. hsp17.9.

CAB36910.1 AJ000691 Quercus suber
 stress protein chaperone. heat shock protein 17.4. hsp17.

CAA63901.1 X94191 Pennisetum glaucum
 heat shock protein 17.0. hsp17.0.

AAC78392.1 U83669 Oryza sativa
 low molecular mass heat shock protein Oshsp17.3. OSHSP17.3. class I LMMHSP.

BAA02160.1 D12635 Oryza sativa
 'low molecular weight heat shock protein'.

AAC78393.1 U83670 Oryza sativa
 low molecular mass heat shock protein Oshsp18.0. OSHSP18.0. class I LMMHSP.

CAA31785.1 X13431 Triticum aestivum
 put. heat shock protein (AA 1 -151).

CAA63570.1 X92983 Pseudotsuga menziesii
 low molecular weight heat-shock protein.

AAC78394.1 U83671 Oryza sativa
 low molecular mass heat shock protein Oshsp17.7. OSHSP17.7. class I LMMHSP.

CAA63571.1 X92984 Pseudotsuga menziesii
 low molecular weight heat-shock protein.

SEQ ID NO: 901

AAG08959.1 AF122051 Solanum tuberosum
 tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.

AAG08960.1 AF122052 Solanum tuberosum
 tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.

AAG08961.1 AF122053 Solanum tuberosum
 tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.

AAF67053.1 AF190304 Adiantum raddianum
 c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.

AAF67052.1 AF190303 Adiantum raddianum
 c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.

AAF34434.1 AF172282 Oryza sativa
 myb-like protein. DUPR11.29.

AAF78888.1	AF189786	<i>Physcomitrella patens</i>
putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.		
AAF78887.1	AF189785	<i>Physcomitrella patens</i>
putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.		
AAF43043.1	AF236059	<i>Papaver rhoes</i>
putative Myb-related domain. pmr.		
BAA94769.1	AP001859	<i>Oryza sativa</i>
Similar to <i>Arabidopsis thaliana</i> chromosome 4, BAC clone F4D11; putative myb-protein. (AL022537).		
AAF78890.1	AF189788	<i>Hordeum vulgare</i>
putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.		
AAF78889.1	AF189787	<i>Hordeum vulgare</i>
putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.		
BAA88169.1	AP000836	<i>Oryza sativa</i>
Similar to putative transcription factor (AF062890).		
BAA88205.1	AP000837	<i>Oryza sativa</i>
Similar to putative transcription factor (AF062890).		
CAA78388.1	Z13998	<i>Petunia x hybrida</i>
DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.		
AAF67051.1	AF190302	<i>Secale cereale</i>
c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.		
AAF67050.1	AF190301	<i>Secale cereale</i>
c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.		
AAG28525.1	AF198498	<i>Nicotiana tabacum</i>
anther-specific myb-related protein 2. mybAS2. NtMYBAS2; contains tandem R2, R3 myb domains similar to c-myb family.		
BAB12688.1	AP002746	<i>Oryza sativa</i>
putative MYB family transcription factor. P0671B11.3. contains ESTs AU082307(E0784),C72014(E0784).		
BAA99440.1	AP002743	<i>Oryza sativa</i>
putative MYB family transcription factor. P0710E05.27. contains ESTs AU082307(E0784),C72014(E0784).		
AAK19619.1	AF336286	<i>Gossypium hirsutum</i>
GHMYB9. ghmyb9. similar to myb.		
CAA64615.1	X95297	<i>Lycopersicon esculentum</i>
transcription factor. THM1. myb-related.		
BAA81730.1	AB029159	<i>Glycine max</i>
GmMYB29A1.		
CAA50224.1	X70879	<i>Hordeum vulgare</i>
MybHv1. myb1.		
CAA50222.1	X70877	<i>Hordeum vulgare</i>
MybHv1. myb1.		

CAB40189.1	AJ133638	<i>Avena sativa</i> transcriptional activator. myb protein. gamyb.
AAG28526.1	AF198499	<i>Nicotiana tabacum</i> anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
AAD31395.1	AF114162	<i>Lolium temulentum</i> gibberellin MYB transcription factor. GAMyb. R2/R3-MYB.
BAA81732.1	AB029161	<i>Glycine max</i> GmMYB29A2.
BAA81731.1	AB029160	<i>Glycine max</i> GmMYB29A1.
CAA61021.1	X87690	<i>Hordeum vulgare</i> transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.
AAG22863.1	AY008692	<i>Hordeum vulgare</i> transcription factor GAMyb. Gamyb.
BAA96421.1	AB044084	<i>Triticum aestivum</i> transcription activator for gibberellin response. GAMyb protein. Ta-GAMyb.
BAA81733.2	AB029162	<i>Glycine max</i> GmMYB29A2.
BAA81736.1	AB029165	<i>Glycine max</i> GmMYB29B2.
AAA33067.1	L04497	<i>Gossypium hirsutum</i> MYB A; putative.
BAB39972.1	AP003018	<i>Oryza sativa</i> putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).
CAA72218.1	Y11415	<i>Oryza sativa</i> myb.
CAA67000.1	X98355	<i>Oryza sativa</i> activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.
BAB39987.1	AP003020	<i>Oryza sativa</i> putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
CAA78387.1	Z13997	<i>Petunia x hybrida</i> DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
CAA72217.1	Y11414	<i>Oryza sativa</i> myb.
BAA23341.1	D88621	<i>Oryza sativa</i> transfactor. OSMYB5. Osmyb5.

BAA93038.1	AP001552	Oryza sativa EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
CAA64614.1	X95296	Lycopersicon esculentum transcription factor. THM27. myb-related.
AAK19616.1	AF336283	Gossypium hirsutum GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.
CAA78386.1	Z13996	Petunia x hybrida DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
CAA67575.1	X99134	Lycopersicon esculentum transcription factor. THM6. myb-related.
BAA88222.1	AB028650	Nicotiana tabacum myb-related transcription factor LBM2. lbm2.
		SEQ ID NO: 902
CAA57773.1	X82329	Arachis hypogaea chitinase (class II). chi2;1.
AAD54935.1	AF141373	Petroselinum crispum random hydrolysis of 1,4-beta-acetamido-2-deoxy-D-glucoside linkages in chitin. chitinase precursor. Chi2-1. class II.
AAD54936.1	AF141374	Petroselinum crispum random hydrolysis of 1,4-beta-acetamido-2-deoxy-D-glucoside linkages in chitin. chitinase precursor. Chi2-2. class II.
AAF00131.1	AF147091	Fragaria x ananassa chitin degradation. class II chitinase. Chi2-1.
AAC95376.1	AF105426	Cynodon dactylon chitinase. Cht2.
BAA95846.1	AP002070	Oryza sativa Similar to Oryza sativa clone RGCH7 chitinase. (AF013581).
AAA32986.1	M95835	Brassica napus endochitinase. Ch25.
AAF69783.1	AF135143	Arabis lemmonii class I chitinase.
AAF69775.1	AF135135	Arabis drummondii class I chitinase.
AAF69792.1	AF135152	Arabis parishii class I chitinase.
AAC95375.1	AF105425	Cynodon dactylon chitinase. Cht1.
AAF69785.1	AF135145	Arabis lignifera class I chitinase.

AAF69770.1	AF135130	Arabis holboellii class I chitinase.
AAF69781.1	AF135141	Arabis gunnisoniana class I chitinase.
AAF69777.1	AF135137	Arabis fecunda class I chitinase.
AAF69790.1	AF135150	Arabis microphylla class I chitinase.
AAF69787.1	AF135147	Arabis lignifera class I chitinase.
AAF69772.1	AF135132	Arabis gunnisoniana class I chitinase.
AAF69782.1	AF135142	Halimolobos perplexa var. perplexa class I chitinase.
AAF69784.1	AF135144	Arabis lemmonii class I chitinase.
AAF69788.1	AF135148	Arabis lyallii class I chitinase.
BAA03750.1	D16222	Oryza sativa endochitinase. Cht-2.
AAF69776.1	AF135136	Arabis fecunda class I chitinase.
CAA40107.1	X56787	Oryza sativa chitinase.
BAB13369.1	AB048531	Psophocarpus tetragonolobus class I chitinase.
AAF69778.1	AF135138	Arabis glabra class I chitinase.
AAF69786.1	AF135146	Arabis lignifera class I chitinase.
BAA82826.1	AB023464	Arabis gemmifera basic endochitinase. ChiB.
AAF69773.1	AF135133	Arabis blepharophylla class I chitinase.
AAF69791.1	AF135151	Arabis microphylla class I chitinase.
AAF69793.1	AF135153	Arabis parishii class I chitinase.
CAA39535.1	X56063	Oryza sativa chitinase.
BAA03749.1	D16221	Oryza sativa endochitinase. Cht-1.

AAF69789.1	AF135149	<i>Arabis microphylla</i> class I chitinase.
CAA71402.1	Y10373	<i>Medicago truncatula</i> chitinase.
AAC16010.1	AF061805	<i>Elaeagnus umbellata</i> acidic chitinase.
CAA53626.1	X76041	<i>Triticum aestivum</i> endochitinase. CHI.
BAA33971.1	AB008892	<i>Nicotiana tabacum</i> chitinase 134. Chn134.
CAA47921.1	X67693	<i>Solanum tuberosum</i> chitinase. SK2. endochitinase.
AAF69780.1	AF135140	<i>Arabis glabra</i> class I chitinase.
BAB18519.1	AB051578	<i>Secale cereale</i> seed chitinase-a. rsca.
AAA51377.1	L37289	<i>Oryza sativa</i> chitinolytic activity, antifungal activity. chitinase.
AAB41324.1	U83591	<i>Medicago sativa</i> class I chitinase.
CAC17793.1	AJ301671	<i>Nicotiana sylvestris</i> hydrolysis of chitin. endochitinase. chnb. class I chitinase.
AAB41325.1	U83592	<i>Medicago sativa</i> class I chitinase.
AAB23263.1	S43926	<i>Phaseolus vulgaris</i> chitinase. CH5B. This sequence comes from Fig. 1.
AAA33756.1	M13968	<i>Phaseolus vulgaris</i> chitinase (EC 3.2.1.14).
CAA35945.1	X51599	<i>Nicotiana tabacum</i> chitinase. CHN50.
AAA34070.1	M15173	<i>Nicotiana tabacum</i> endochitinase precursor (EC 3.2.1.14).
CAA45822.1	X64519	<i>Nicotiana tabacum</i> chitinase B class I. CHN200.

SEQ ID NO: 903

BAA78764.1	AB023482	<i>Oryza sativa</i> ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to <i>Arabidopsis thaliana</i> APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAF43496.1	AF131222	<i>Lophopyrum elongatum</i> protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	<i>Lophopyrum elongatum</i> protein kinase. ESI47.

AAG16628.1	AY007545	Brassica napus protein serine/threonine kinase BNK1.
BAA94509.1	AB041503	Populus nigra protein kinase 1. PnPK1.
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAA94510.1	AB041504	Populus nigra protein kinase 2. PnPK2.
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAB03429.1	AP002817	Oryza sativa EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB21240.1	AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
CAB51834.1	00069	Oryza sativa I1332.5. contains eukaryotic protein kinase domain PF.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
AAG03090.1	AC073405	Oryza sativa Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAB19337.1	AP003044	Oryza sativa putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
BAA90808.1	AP001168	Oryza sativa Similar to putative receptor-like protein kinase (AL035679).
AAG59657.1	AC084319	Oryza sativa putative protein kinase. OSJNBa0004B24.20.
AAB47424.1	U59317	Lycopersicon pimpinellifolium serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.

AAC48932.1	U13923	Lycopersicon pimpinellifolium Fen. putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.
AAF76307.1	AF220602	Lycopersicon pimpinellifolium Fen kinase.
BAA92221.1	AP001278	Oryza sativa Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	Oryza sativa Similar to putative Ser/Thr protein kinase. (AC004218).
AAB61708.1	U93048	Daucus carota somatic embryogenesis receptor-like kinase. SERK.
AAK11566.1	AF318490	Lycopersicon hirsutum Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
AAK11568.1	AF318492	Lycopersicon hirsutum Pto-like protein kinase B. LhirPtoB.
AAD21872.1	AF078082	Phaseolus vulgaris receptor-like protein kinase homolog RK20-1.
AAF66615.1	AF142596	Nicotiana tabacum LRR receptor-like protein kinase.
AAC23542.1	U20948	Ipomoea trifida receptor protein kinase. IRK1.
AAF91337.1	AF249318	Glycine max Pt1 kinase-like protein. Pt1b. protein kinase.
AAC27894.1	AF023164	Zea mays leucine-rich repeat transmembrane protein kinase 1. ltk1.
AAF76314.1	AF220603	Lycopersicon esculentum Fen kinase. Lescfen.
AAB47422.1	U59318	Lycopersicon esculentum serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.
AAF76313.1	AF220603	Lycopersicon esculentum Pto kinase. LescPth5.
AAB47421.1	U59316	Lycopersicon esculentum serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAF91336.1	AF249317	Glycine max Pt1 kinase-like protein. Pt1a. protein kinase.
AAK11567.1	AF318491	Lycopersicon hirsutum Pto-like protein kinase F. LhirPtoF.
AAC61805.1	U28007	Lycopersicon esculentum serine/threonine protein kinase. Pto kinase interactor 1. Pt1. Pt1 kinase.

AAB93834.1	U82481	Zea mays KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA97692.1	Z73295	Catharanthus roseus receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
CAA73134.1	Y12531	Brassica oleracea serine/threonine kinase. BRLK.
AAF76306.1	AF220602	Lycopersicon pimpinellifolium Pto kinase.
AAB47423.1	U59315	Lycopersicon pimpinellifolium serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
BAB21241.1	AP002953	Oryza sativa Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721), D48017(S13927).
AAC48914.1	U02271	Lycopersicon pimpinellifolium protein kinase.
SEQ ID NO: 904		
AAF65545.1	AF233894	Perilla citriodora limonene synthase.
AAG31437.1	AF241792	Perilla frutescens limonene synthase.
AAK06663.1	AF317695	Perilla frutescens var. frutescens limonene synthase.
AAG31435.1	AF241790	Perilla citriodora limonene synthase.
BAA21629.1	AB005744	Perilla frutescens catalyzing the cyclization of geranyl pyrophosphate to 1-limonene. 1-limonene synthase. gPFLC. similar to perilla PFLC-1:DDBJ Acc#D49368.
AAG31438.1	AF241793	Perilla frutescens limonene synthase.
BAA08367.1	D49368	Perilla frutescens limonene cyclase.
AAC37366.1	L13459	Mentha spicata 4S-limonene synthase.
AAD50304.1	AF175323	Mentha longifolia limonene synthase. monoterpane synthase.
AAG01140.1	AF282875	Schizonepeta tenuifolia (+)-4R-limonene synthase.
AAF21053.1	AF212433	Capsicum annuum UV-induced sesquiterpene cyclase. SC2.

BAA82141.1 AB023816 Solanum tuberosum
vetispiradiene synthase. PVS4. potato sesquiterpene cyclase.

AAF74977.1 AF270425 Gossypium hirsutum
(E,E)-farnesyl diphosphate cyclase. (+)-delta-cadinene synthase. cdn2. sesquiterpene cyclase.

BAA82092.1 AB022598 Solanum tuberosum
vetispiradiene synthase. PVS1. potato sesquiterpene cyclase.

BAA82109.1 AB022720 Solanum tuberosum
vetispiradiene synthase. PVS3. potato sesquiterpene cyclase; PVS3.

AAG09949.1 AF171216 Lycopersicon esculentum
vetispiradiene synthase. LEVS2. sesquiterpene cyclase.

BAA82108.1 AB022719 Solanum tuberosum
vetispiradiene synthase. PVS2. potato sesquiterpene cyclase; PVS2.

AAC12784.1 U88318 Gossypium hirsutum
(E,E)-farnesyl diphosphate cyclizing. (+)-delta-cadinene synthase. cdn1. sesquiterpene cyclase; delta-cadinene synthase.

AAK15641.1 AF326117 Capsicum annuum
sesquiterpene cyclase. PSC2.

AAC61260.1 AF061285 Capsicum annuum
sesquiterpene cyclase. UV induced.

AAG24640.2 AF304444 Artemisia annua
sesquiterpene cyclase.

CAC12731.1 AJ271792 Artemisia annua
putative sesquiterpene cyclase. cASC125.

SEQ ID NO: 905

AAF64450.1 AF239928 Euphorbia esula
glutathione S-transferase. similar to auxin-inducible GST.

AAG34803.1 AF243368 Glycine max
glutathione S-transferase GST 13.

AAG16759.1 AY007561 Lycopersicon esculentum
putative glutathione S-transferase T4.

AAG34798.1 AF243363 Glycine max
glutathione S-transferase GST 8.

AAG34797.1 AF243362 Glycine max
glutathione S-transferase GST 7.

AAG16758.1 AY007560 Lycopersicon esculentum
putative glutathione S-transferase T3.

AAG34809.1 AF243374 Glycine max
glutathione S-transferase GST 19.

AAG34801.1 AF243366 Glycine max
glutathione S-transferase GST 11.

AAG34796.1 AF243361 Glycine max
glutathione S-transferase GST 6.

AAG34807.1 AF243372 Glycine max
glutathione S-transferase GST 17.

AAG16757.1 AY007559 Lycopersicon esculentum
putative glutathione S-transferase T2.

AAG16756.1 AY007558 Lycopersicon esculentum
putative glutathione S-transferase T1.

AAG34804.1 AF243369 Glycine max
glutathione S-transferase GST 14.

AAG34810.1 AF243375 Glycine max
glutathione S-transferase GST 20.

AAG34808.1 AF243373 Glycine max
glutathione S-transferase GST 18.

AAG34805.1 AF243370 Glycine max
glutathione S-transferase GST 15.

AAG34844.1 AF244701 Zea mays
glutathione S-transferase GST 36.

AAG34829.1 AF244686 Zea mays
glutathione S-transferase GST 21.

AAG34831.1 AF244688 Zea mays
glutathione S-transferase GST 23.

AAA68430.1 J03679 Solanum tuberosum
glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.

AAC18566.1 AF048978 Glycine max
2,4-D inducible glutathione S-transferase. GSTa.

AAG34832.1 AF244689 Zea mays
glutathione S-transferase GST 24.

AAG34800.1 AF243365 Glycine max
glutathione S-transferase GST 10.

AAG34849.1 AF244706 Zea mays
glutathione S-transferase GST 41.

AAG34837.1 AF244694 Zea mays
glutathione S-transferase GST 29.

AAC32118.1 AF051214 Picea mariana
probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.

AAG41204.1 AF321437 Suaeda maritima
glutathione transferase.

AAG34802.1 AF243367 Glycine max
glutathione S-transferase GST 12.

AAF29773.1 AF159229 Gossypium hirsutum
glutathione S-transferase. GST.

AAG32472.1 AF309379 Oryza sativa subsp. japonica
putative glutathione S-transferase OsGSTU3.

AAG34836.1 AF244693 Zea mays
glutathione S-transferase GST 28.

CAA04391.1 AJ000923 Carica papaya
glutathione transferase. PGST1.

CAA71784.1 Y10820 Glycine max
glutathione transferase.

CAA09187.1 AJ010448 Alopecurus myosuroides
glutathione transferase. GST1a.

AAG34795.1 AF243360 Glycine max
glutathione S-transferase GST 5.

CAA09188.1 AJ010449 Alopecurus myosuroides
glutathione transferase. GST1b.

AAG34806.1 AF243371 Glycine max
glutathione S-transferase GST 16.

CAC24549.1 AJ296343 Cichorium intybus x Cichorium endivia
glutathione S-transferase. chi-GST1. auxin-induced GST.

AAC28101.1 AF079511 Mesembryanthemum crystallinum
glutathione S-transferase.

SEQ ID NO: 907

AAA33280.1 L20475 Datura stramonium
29kDa protein; high homology to aa sequence of tropinone reductases.

AAA33281.1 L20473 Datura stramonium
catalyses a stereospecific reduction of tropinone to tropine. tropinone reductase-I.

CAC34420.1 AJ307584 Solanum tuberosum
tropine forming tropinone reductase. tropinone reductase I. TRI.

BAA85844.1 AB026544 Hyoscyamus niger
tropinone reductase-I. tr1.

BAA13547.1 D88156 Hyoscyamus niger
tropinone reductase-I.

AAA33282.1 L20474 Datura stramonium
catalyses a stereospecific reduction of tropinone to pseudotropine. tropinone reductase-II.

AAB09776.1 L20485 Hyoscyamus niger
tropinone reductase-II.

BAA85845.1 AB026545 Hyoscyamus niger
tropinone reductase-II. tr2.

CAB52307.1 AJ245634 Solanum tuberosum
pseudotropine forming tropinone reductase. tropinone reductase II. TRII.

CAC19810.1 AJ292343 Solanum tuberosum
pseudotropine forming tropinone reductase. tropinone reductase II. trII.

CAA45866.1 X64566 Cuphea lanceolata
beta-ketoacyl-ACP reductase. Clkr27. 3-oxoacyl-[acyl-carrier protein] reductase.

CAA45793.1	X64463	Brassica napus 3-oxoacyl-[acyl-carrier protein] reductase.
AAB82767.1	U89509	Zea mays cuticular wax biosynthesis. b-keto acyl reductase. glossy8.
AAB82766.1	U89510	Hordeum vulgare cuticular wax biosynthesis. b-keto acyl reductase. glossy8.
CAA74176.1	Y13861	Nicotiana tabacum enoyl-ACP reductase. enr-T2.
AAB20114.2	S60064	Brassica napus enoyl-acyl carrier protein reductase. This sequence comes from fig3; conceptual translation differs from published sequence.
CAA74177.1	Y13862	Nicotiana tabacum enoyl-ACP reductase. enr-T1.
AAC78100.1	AF093628	Oryza sativa protochlorophyllide reductase homolog.
CAA05879.1	AJ003124	Petunia x hybrida enoyl-ACP reductase. pte.
CAA64729.1	X95462	Brassica napus enoyl reductase.
CAA05816.1	AJ003025	Oryza sativa enoyl-ACP reductase.
BAA99570.1	AB036823	Chlorella vulgaris oxidoreductase. oxi.
SEQ ID NO: 909		
BAA82107.1	AB022693	Nicotiana tabacum transcription factor. NtWRKY1.
AAC31956.1	AF080595	Pimpinella brachycarpa zinc finger protein. ZFP1. WRKY1.
AAD55974.1	AF121353	Petroselinum crispum zinc-finger type transcription factor WRKY1. WRKY1.
BAA77383.1	AB020590	Nicotiana tabacum transcription factor NtWRKY2.
AAC49527.1	U48831	Petroselinum crispum WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.
AAD32677.1	AF140554	Avena sativa DNA-binding protein WRKY1. wrky1. putative transcription factor.
CAA88326.1	Z48429	Avena fatua binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAD16139.1	AF096299	Nicotiana tabacum DNA-binding protein 2. WRKY2. transcription factor.
BAA86031.1	AB026890	Nicotiana tabacum transcription factor NtWRKY4.

AAC37515.1	L44134	Cucumis sativus SPF1-like DNA-binding protein.
AAK16171.1	AC079887	Oryza sativa putative DNA-binding protein. OSJNBa0040E01.10.
AAF23898.1	AF193802	Oryza sativa zinc finger transcription factor WRKY1.
AAD16138.1	AF096298	Nicotiana tabacum DNA-binding protein 1. WRKY1. transcription factor.
AAC49529.1	U58540	Petroselinum crispum WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
CAB97004.1	AJ278507	Solanum tuberosum putative transcription factor. WRKY DNA binding protein. WRKY1.
BAB19075.1	AP002744	Oryza sativa putative DNA-binding protein homolog. P0006C01.17.
BAB19096.1	AP002839	Oryza sativa putative DNA-binding protein homolog. P0688A04.2.
AAK16170.1	AC079887	Oryza sativa putative DNA binding protein. OSJNBa0040E01.4.
BAB40073.1	AP003074	Oryza sativa putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
AAD38283.1	AC007789	Oryza sativa putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAB18313.1	AP002865	Oryza sativa putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
CAA88331.1	Z48431	Avena fatua binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAC49528.1	U56834	Petroselinum crispum DNA-binding. WRKY3. WRKY-type DNA-binding protein.
AAG35658.1	AF204925	Petroselinum crispum transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.
BAB16432.1	AB041520	Nicotiana tabacum WRKY transcription factor Nt-SubD48. Nt-SubD48.
AAD32676.1	AF140553	Avena sativa DNA-binding protein WRKY3. wrky3. putative transcription factor.
AAG46150.1	AC018727	Oryza sativa putative DNA-binding protein. OSJNBa0056G17.18.
BAA77358.1	AB020023	Nicotiana tabacum WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.
AAG35659.1	AF204926	Petroselinum crispum transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.
AAD27591.1	AF121354	Petroselinum crispum binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.

CAB66338.1 AJ279697	Betula pendula wrky-type DNA binding protein. wrky.
AAF61864.1 AF193771	Nicotiana tabacum DNA-binding protein 4. WRKY4. transcription factor.
BAA87069.1 AB035271	Matricaria chamomilla elicitor-induced DNA-binding protein homolog. McWRKY1.
AAF61863.1 AF193770	Nicotiana tabacum DNA-binding protein 3. WRKY3. transcription factor.
SEQ ID NO: 910	
AAC09420.1 M68929	Mitochondrion Marchantia polymorpha rps14.
CAA33994.1 X15901	Plastid Oryza sativa ribosomal protein S14. rps14.
SEQ ID NO: 911	
CAA55128.1 X78325	Nicotiana tabacum chitinase/lysozyme. Pz.
CAA54373.1 X77110	Nicotiana tabacum chitinase, class V. chi-V.
CAA54374.1 X77111	Nicotiana tabacum chitinase, class V. chi-V.
SEQ ID NO: 912	
CAB55394.1 AL117264	Oryza sativa zwh0010.1. similar to Arabidopsis germin-like protein 6 (AF032976); Method: conceptual translation with partial peptide sequencing.
BAA78563.1 AB024338	Atriplex lentiformis germin-like protein.
AAB97470.1 AF042489	Oryza sativa germin-like protein 16. glp16.
AAA33030.1 M93041	Mesembryanthemum crystallinum germin-like protein. germin-like protein.
CAB65371.1 AJ250834	Pisum sativum germin-like protein. ger2b. 2nd variant of the clone PsGER2.
CAB55559.1 AJ237943	Triticum aestivum germin-like protein. glp2b.
CAB65370.1 AJ250833	Pisum sativum germin-like protein. ger2a. 1st variant of this clone.
CAB55558.1 AJ237942	Triticum aestivum germin-like protein. glp2a.
AAD43971.1 AF141878	Oryza sativa germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.

AAD43973.1	AF141880	Oryza sativa germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.
AAC04837.1	AF032976	Oryza sativa germin-like protein 6. GER6. similar to wheat and barley oxalate oxidase.
AAG00425.1	AF250933	Hordeum vulgare germin A. GerA. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAD43972.1	AF141879	Oryza sativa germin-like protein 2 precursor. RGLP2. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.
CAA63659.1	X93171	Hordeum vulgare oxalate oxidase-like protein or germin-like protein.
AAC04833.1	AF032972	Oryza sativa germin-like protein 2. GER2. similar to wheat and barley oxalate oxidase.
AAC04834.1	AF032973	Oryza sativa germin-like protein 3. GER3. similar to wheat and barley oxalate oxidase.
AAC04832.1	AF032971	Oryza sativa germin-like protein 1. GER1. similar to wheat and barley oxalate oxidase.
AAG00426.1	AF250934	Hordeum vulgare germin B. GerB. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAG00427.1	AF250935	Hordeum vulgare germin F. GerF. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAF34811.1	AF005084	Triticum aestivum oxalate oxidase. up-regulated by aluminum.
AAC04835.1	AF032974	Oryza sativa germin-like protein 4. GER4. similar to wheat and barley oxalate oxidase.
BAB39965.1	AP003018	Oryza sativa probable germin protein 4. OSJNBa0004B13.19. contains ESTs AU101991(S4037),AU070167(R0031).
BAB39980.1	AP003020	Oryza sativa probable germin protein 4. P0498A12.8. contains ESTs AU101991(S4037),AU070167(R0031).
AAG00428.1	AF250936	Hordeum vulgare germin D. GerD. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAA20245.1	U01963	Hordeum vulgare germin subunit.
CAC19429.1	AJ291825	Lolium perenne oxalate oxidase. oxO1.
AAA34270.1	M63223	Triticum aestivum germin. germin 9f-2.8.
AAA34268.1	M21962	Triticum aestivum germin protein precursor.

CAA74595.1	Y14203	Hordeum vulgare oxalate oxidase.
AAG00429.1	AF250937	Hordeum vulgare germin E. GerE. apoplastic protein.
CAB65369.1	AJ250832	Pisum sativum germin-like protein. ger1.
AAA32959.1	L15737	Hordeum vulgare oxalate oxidase. This is the sequence of the complete mature peptide.
CAA71052.1	Y09917	Triticum aestivum germin homolog. pSBGer3.
AAA34271.1	M63224	Triticum aestivum germin. germin 9f-3.8.
CAA71050.1	Y09915	Triticum aestivum germin homolog. pSBGer1.
BAB18339.1	AP002865	Oryza sativa putative germin protein. P0034C11.30. contains EST C97263(C53484).
AAD38298.1	AC007789	Oryza sativa putative oxalate oxidase (germin protein). OSJNBa0049B20.25.
BAA86880.1	AB028454	Barbula unguiculata germin-like protein.
AAF03355.1	AF132671	Nicotiana plumbaginifolia nectarin I precursor. NEC1. germin-like protein.
BAA25197.1	AB012138	Lycopersicon esculentum adaptation to Mn-deficiency. germin-like protein. Mdip1.
AAC78470.1	AF067731	Solanum tuberosum germin-like protein. OXAOXA. similar to oxalate oxidase.
AAC25777.1	AF072694	Oryza sativa germin-like protein 7. GER7. similar to wheat and barley oxalate oxidase.
AAC99473.1	AF039201	Pinus caribaea germin-like protein. PCGER1.
CAA71051.1	Y09916	Triticum aestivum germin homolog. pSBGer2.
AAC05146.1	AF049065	Pinus radiata germin-like protein. PRGer1.
CAC34417.1	AJ311624	Pisum sativum Germin-like protein. glp3.
SEQ ID NO: 915		
BAB19363.1	AP002542	Oryza sativa putative beta-1,3-glucanase. P0679C08.2.
AAD10386.1	U72255	Oryza sativa beta-1,3-glucanase precursor. Gns9.

CAB85903.1	AJ251646	Pisum sativum hydrolysis of beta-1,3 conjugated glucans. beta-1,3 glucanase. gns2.
AAA90953.1	U30323	Triticum aestivum beta 1,3-glucanase. Glc1.
BAA89481.1	AB029462	Salix gilgiana beta-1,3-glucanase. SgGN1.
BAB40807.1	AB052291	Pyrus pyrifolia catalyzing the hydrolysis of 1,3-beta-glucosyl linkages. endo-1,3-beta-glucanase-like protein. bgn-1. Amino acid alignment of the protein(BGN-1) encoded by pear pollen bgn-1 with barley endo-1,3-beta-glucanase(GII. accession number:pdb/1GHS-B/2.3/2/306/N/)(40% identity) and their hydrophobic cluster analysis(HCA)(a overall HCA homology score of 87.1%) showed that it was most likely that the bgn-1 encoded a endo-1,3-beta-glucanase. A higher identity(59.3%) was found between BGN-1 and a putative pea endo-1,3-beta-glucanase (accession number:dad/AJ251646-1).
AAB82772.2	AF001523	Musa acuminata beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
CAA49513.1	X69887	Brassica napus beta-1,3-glucanase homologue.
AAF08679.1	AF004838	Musa acuminata beta-1,3-glucanase.
CAA82271.1	Z28697	Nicotiana tabacum beta-1,3-glucanase.
AAD10384.1	U72253	Oryza sativa beta-1,3-glucanase precursor. Gns7.
CAB71021.1	AJ271598	Hieracium piloselloides putative role in callose degradation. putative beta-1,3-glucanase. gluc.
CAA30261.1	X07280	Nicotiana plumbaginifolia beta-glucanase.
AAA51643.1	M23120	Nicotiana plumbaginifolia beta-glucanase precursor.
AAA87456.1	U22147	Hevea brasiliensis beta-1,3-glucanase. HGN1. hydrolytic enzyme.
AAA34078.1	M63634	Nicotiana plumbaginifolia regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.
AAD10385.1	U72254	Oryza sativa beta-1,3-glucanase precursor. Gns8.
CAB38443.1	AJ133470	Hevea brasiliensis beta-1,3-glucanase. hgn1.
AAB03501.1	U41323	Glycine max beta-1,3-glucanase. SGN1.
AAA32939.1	M62907	Hordeum vulgare hydrolysis of beta-(1-3)-glucan. (1-3)-beta-glucanase. cBGL32.

AAD33881.1	AF141654	Nicotiana tabacum beta-1,3-glucanase. GGL4.
AAA03617.1	M80604	Lycopersicon esculentum beta-1,3-glucanase.
BAA77786.1	AB027431	Oryza sativa beta-1,3-glucanase.
BAA77787.1	AB027432	Oryza sativa beta-1,3-glucanase.
CAB91554.1	AJ277900	Vitis vinifera beta 1-3 glucanase. g1.
AAC14399.1	AF030771	Hordeum vulgare beta-1,3-glucanase 2. BGL32.
CAA03908.1	AJ000081	Citrus sinensis glucan hydrolase. beta-1,3-glucanase. gns1.
AAG24921.1	AF311749	Hevea brasiliensis beta-1,3-glucanase.
AAA33946.1	M37753	Glycine max beta-1,3-endoglucanase (EC 3.2.1.39).
AAA63542.1	M59443	Nicotiana tabacum acidic beta-1,3-glucanase. glucanase.
AAD28732.1	AF112965	Triticum aestivum beta-1,3-glucanase precursor. Glb3.
AAD10381.1	U72250	Oryza sativa beta-1,3-glucanase precursor. Gns4.
CAA57255.1	X81560	Nicotiana tabacum (1-)-beta-glucanase. Sp41a.
AAD33880.1	AF141653	Nicotiana tabacum beta-1,3-glucanase. GGL1.
AAB86541.1	AF030166	Oryza sativa glucanase. glu1.
AAA63539.1	M60402	Nicotiana tabacum glucan beta-1,3-glucanase. glucanase GLA.
AAA34053.1	M60464	Nicotiana tabacum beta-1,3-glucanase.
AAD10380.1	U72249	Oryza sativa beta-1,3-glucanase precursor. Gns3.
AAA63540.1	M60403	Nicotiana tabacum glucan-1,3-beta-glucosidase. glucanase GLB.
SEQ ID NO: 916		
AAA85440.1	U32624	Sorghum bicolor cytochrome P-450. CYP79. P450TYR; N-hydroxylase.

AAF27289.1	AF140613	<i>Manihot esculenta</i> N-hydroxylating cytochrome P450. CYP79D1.
AAF27290.1	AF140614	<i>Manihot esculenta</i> N-hydroxylating cytochrome P450. CYP79D2.
AAD03415.1	AF069494	<i>Sinapis alba</i> converts tyrosine to para-hydrophenylacetaldoxime in para-hydroxybenzylglucosinolate biosynthesis. cytochrome P450. CYP79B1.
AAG59648.1	AC084319	<i>Oryza sativa</i> putative cytochrome p450tyr. OSJNBa0004B24.15.
AAF66543.1	AF140609	<i>Triglochin maritimum</i> cytochrome P450 CYP79E1. CYP79E1.
AAF66544.1	AF140610	<i>Triglochin maritimum</i> cytochrome P450 CYP79E2. CYP79E2.
BAA92894.1	AB006790	<i>Petunia x hybrida</i> cytochrome P450. IMT-2.
AAB94587.1	AF022458	<i>Glycine max</i> CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAC32274.1	AF081575	<i>Petunia x hybrida</i> flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.
AAD56282.1	AF155332	<i>Petunia x hybrida</i> flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
CAA64635.1	X95342	<i>Nicotiana tabacum</i> cytochrome P450. hsr515. hypersensitivity-related gene.
CAA50155.1	X70824	<i>Solanum melongena</i> flavonoid hydroxylase (P450). CYP75.
AAG44132.1	AF218296	<i>Pisum sativum</i> cytochrome P450. P450 isolog.
AAA32913.1	M32885	<i>Persea americana</i> cytochrome P-450LXXIA1 (cyp71A1).
BAA84071.1	AB028151	<i>Antirrhinum majus</i> flavone synthase II. cytochrome P450. AFNS2.
AAD38930.1	AF135485	<i>Glycine max</i> cytochrome P450 monooxygenaseCYP93D1. CYP93E1.
AAB17562.1	U72654	<i>Eustoma grandiflorum</i> flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
AAG34695.1	AF313492	<i>Matthiola incana</i> putative cytochrome P450.
CAA65580.1	X96784	<i>Nicotiana tabacum</i> cytochrome P450. hsr515.
BAA93634.1	AB025016	<i>Lotus japonicus</i> cytochrome P450.
CAA71513.1	Y10489	<i>Glycine max</i> putative cytochrome P450.

AAB94590.1	AF022461	Glycine max CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
CAA71876.1	Y10982	Glycine max putative cytochrome P450.
BAA12159.1	D83968	Glycine max Cytochrome P-450 (CYP93A1).
AAG14962.1	AF214008	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H2.
BAA74465.1	AB022732	Glycyrrhiza echinata cytochrome P450. CYP Ge-31.
BAA22422.1	AB001379	Glycyrrhiza echinata cytochrome P450. CYP81E1.
AAG14961.1	AF214007	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H1.
CAA04117.1	AJ000478	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'-race).
CAA04116.1	AJ000477	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
AAB94593.1	AF022464	Glycine max CYP77A3p. CYP77A3. cytochrome P450 monooxygenase.
BAA13076.1	D86351	Glycine max cytochrome P-450 (CYP93A2).
CAA50647.1	X71656	Solanum melongena P450 hydroxylase.
SEQ ID NO: 918		
CAA06223.1	AJ004923	Lycopersicon esculentum Squalene epoxidase. ERG.
SEQ ID NO: 919		
AAF71823.1	AF153276	Populus tremula x Populus tremuloides pumilio domain-containing protein PPD1. PPD1. similar to Drosophila pumilio protein RNA-binding domain.
SEQ ID NO: 920		
BAA82393.1	AP000367	Oryza sativa EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).
CAC20842.1	AJ250467	Pinus sylvestris receptor protein kinase. upk.
AAB36558.1	U77888	Ipomoea nil receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.
AAF91324.1	AF244890	Glycine max receptor-like protein kinase 3. RLK3. GmRLK3.

BAB40094.1	AP003210	Oryza sativa putative receptor protein kinase. OSJNBa0010K01.7.
AAF91322.1	AF244888	Glycine max receptor-like protein kinase 1. RLK1. GmRLK1.
AAC36318.1	AF053127	Malus x domestica leucine-rich receptor-like protein kinase. LRPKm1.
BAA84787.1	AP000559	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
BAA83373.1	AP000391	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
AAF59905.1	AF197946	Glycine max receptor protein kinase-like protein. CLV1A.
AAK27806.1	AC022457	Oryza sativa putative protein kinase. OSJNBa0006L06.21.
AAF91323.1	AF244889	Glycine max receptor-like protein kinase 2. RLK2. GmRLK2.
AAF34426.1	AF172282	Oryza sativa leucine rich repeat containing protein kinase. DUPR11.16.
AAK27817.1	AC022457	Oryza sativa putative protein kinase. OSJNBa0006L06.16.
CAA61510.1	X89226	Oryza sativa leucine-rich repeat/receptor protein kinase. lrk2.
BAB03621.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.21.
AAB82755.1	U72725	Oryza longistaminata receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.
BAB03629.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.30.
AAB61708.1	U93048	Daucus carota somatic embryogenesis receptor-like kinase. SERK.
AAF66615.1	AF142596	Nicotiana tabacum LRR receptor-like protein kinase.
AAB82756.1	U72724	Oryza sativa receptor kinase-like protein. Xa21 gene family member E.
CAB51480.1	Y14600	Sorghum bicolor putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
BAB39873.1	AP002882	Oryza sativa putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

BAB18321.1 AP002865	Oryza sativa putative receptor protein kinase. P0034C11.11.
BAB40081.1 AP003074	Oryza sativa putative receptor protein kinase. OSJNBa0004G10.30.
AAD38286.1 AC007789	Oryza sativa putative protein kinase. OSJNBa0049B20.13.
BAB21240.1 AP002953	Oryza sativa Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK21965.1 AY028699	Brassica napus receptor protein kinase PERK1.
BAA87853.1 AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB16871.1 AP002537	Oryza sativa putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAC27894.1 AF023164	Zea mays leucine-rich repeat transmembrane protein kinase 1. ltk1.
AAK00425.1 AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
AAG59657.1 AC084319	Oryza sativa putative protein kinase. OSJNBa0004B24.20.
BAA94519.1 AP001800	Oryza sativa ESTs AU032341(R3918),AU071016(R10613) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4, BAC F9D16; putative receptor kinase (AL035394).
BAB07903.1 AP002835	Oryza sativa putative receptor kinase. P0417G05.10. contains ESTs AU032341(R3918),AU071016(R10613).
SEQ ID NO: 921	
BAA96250.1 AB027617	Pyrus pyrifolia UDP-glucose pyrophosphorylase.
BAA25917.1 AB013353	Pyrus pyrifolia UDP-glucose pyrophosphorylase.
CAA62689.1 X91347	Hordeum vulgare UDP-glucose pyrophosphorylase.
AAF62555.1 AF249880	Oryza sativa subsp. indica UDP-glucose pyrophosphorylase. UDPGase.
SEQ ID NO: 922	
AAD03415.1 AF069494	Sinapis alba converts tyrosine to para-hydrophenylacetaldoxime in para-hydroxybenzylglucosinolate biosynthesis. cytochrome P450. CYP79B1.

AAA85440.1	U32624	Sorghum bicolor cytochrome P-450. CYP79. P450TYR; N-hydroxylase.
AAF27289.1	AF140613	Manihot esculenta N-hydroxylating cytochrome P450. CYP79D1.
AAF27290.1	AF140614	Manihot esculenta N-hydroxylating cytochrome P450. CYP79D2.
AAG59648.1	AC084319	Oryza sativa putative cytochrome p450tyr. OSJNBa0004B24.15.
AAF66543.1	AF140609	Triglochin maritimum cytochrome P450 CYP79E1. CYP79E1.
AAF66544.1	AF140610	Triglochin maritimum cytochrome P450 CYP79E2. CYP79E2.
BAA92894.1	AB006790	Petunia x hybrida cytochrome P450. IMT-2.
AAD56282.1	AF155332	Petunia x hybrida flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
CAA50155.1	X70824	Solanum melongena flavonoid hydroxylase (P450). CYP75.
AAC32274.1	AF081575	Petunia x hybrida flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.
AAG34695.1	AF313492	Matthiola incana putative cytochrome P450.
AAA32913.1	M32885	Persea americana cytochrome P-450LXXIA1 (cyp71A1).
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
CAA65580.1	X96784	Nicotiana tabacum cytochrome P450. hsr515.
AAB94587.1	AF022458	Glycine max CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAB17562.1	U72654	Eustoma grandiflorum flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
AAG09208.1	AF175278	Pisum sativum wound-inducible P450 hydroxylase. CYP82A1.
AAD37433.1	AF150881	Lycopersicon esculentum x Lycopersicon peruvianum catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.
CAA04117.1	AJ000478	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'- race).
CAA04116.1	AJ000477	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

CAB43505.1	AJ239051	Cicer arietinum cytochrome P450. cyp81E2.
AAC49188.2	U29333	Pisum sativum cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
AAG14963.1	AF214009	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H3.
AAD38930.1	AF135485	Glycine max cytochrome P450 monooxygenaseCYP93D1. CYP93E1.
AAG14962.1	AF214008	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H2.
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
AAB94588.1	AF022459	Glycine max CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAG14961.1	AF214007	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H1.
AAB94590.1	AF022461	Glycine max CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
BAA84071.1	AB028151	Antirrhinum majus flavone synthase II. cytochrome P450. AFNS2.
CAA50442.1	X71130	Petunia x hybrida P450 hydroxylase. PET 1.

SEQ ID NO: 924

BAB20581.1	AB042268	Zea mays response regulator 6. ZmRR6.
AAK14395.1	AF339732	Dianthus caryophyllus response regulator protein. RR.
BAB20580.1	AB042267	Zea mays response regulator 5. ZmRR5.
BAB20579.1	AB042261	Zea mays response regulator 4. ZmRR4.
BAA85113.1	AB031012	Zea mays response regulator 2. ZmRR2. cytokinin-inducible.
BAA82873.1	AB024291	Zea mays response regulator. ZmRR2.
BAA75253.1	AB004882	Zea mays response regulator. ZmCip1, cytokinin-inducible protein.
BAA85112.1	AB031011	Zea mays response regulator 1. ZmRR1. cytokinin-inducible.

BAB17300.1 AB042260 Zea mays
response regulator. ZmRR3.

BAB20582.1 AB042269 Zea mays
response regulator 7. ZmRR7.

BAB41137.1 AB060130 Zea mays
response regulator 8. ZmRR8.

SEQ ID NO: 925

AAA33280.1 L20475 Datura stramonium
29kDa protein; high homology to aa sequence of tropinone reductases.

AAA33281.1 L20473 Datura stramonium
catalyses a stereospecific reduction of tropinone to tropine. tropinone reductase-I.

BAA85844.1 AB026544 Hyoscyamus niger
tropinone reductase-I. tr1.

CAC34420.1 AJ307584 Solanum tuberosum
tropine forming tropinone reductase. tropinone reductase I. TRI.

BAA13547.1 D88156 Hyoscyamus niger
tropinone reductase-I.

AAA33282.1 L20474 Datura stramonium
catalyses a stereospecific reduction of tropinone to pseudotropine. tropinone reductase-II.

BAA85845.1 AB026545 Hyoscyamus niger
tropinone reductase-II. tr2.

AAB09776.1 L20485 Hyoscyamus niger
tropinone reductase-II.

CAB52307.1 AJ245634 Solanum tuberosum
pseudotropine forming tropinone reductase. tropinone reductase II. TRII.

CAC19810.1 AJ292343 Solanum tuberosum
pseudotropine forming tropinone reductase. tropinone reductase II. trII.

CAA45866.1 X64566 Cuphea lanceolata
beta-ketoacyl-ACP reductase. Clkr27. 3-oxoacyl-[acyl-carrier protein] reductase.

CAA45793.1 X64463 Brassica napus
3-oxoacyl-[acyl-carrier protein] reductase.

AAB82767.1 U89509 Zea mays
cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAB82766.1 U89510 Hordeum vulgare
cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAB20114.2 S60064 Brassica napus
enoyl-acyl carrier protein reductase. This sequence comes from fig3; conceptual translation
differs from published sequence.

CAA74176.1 Y13861 Nicotiana tabacum
enoyl-ACP reductase. enr-T2.

AAB82764.1 U89511 Allium porrum
cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAC78100.1 AF093628 Oryza sativa
protochlorophyllide reductase homolog.

CAA74177.1 Y13862 Nicotiana tabacum
enoyl-ACP reductase. enr-T1.

SEQ ID NO: 927

AAD43046.1 AF124045 Sorghum bicolor
GTP-binding protein-like. 110K5.8. terminal exon, defined by homology to maize ESTs.

SEQ ID NO: 928

CAA09619.1 AJ011418 Lycopersicon esculentum
ubiquitin activating enzyme.

AAC32140.1 AF051239 Picea mariana
probable ubiquitin activating enzyme 2. Sb53. similar to Arabidopsis thaliana ubiquitin
activating enzyme 2 encoded by GenBank Accession Number U40566.

AAA34308.1 M55604 Triticum aestivum
ubiquitin-activating enzyme E1. UBA1.

AAA34265.1 M90663 Triticum aestivum
ubiquitin activating enyme. E1.

AAA34266.1 M90664 Triticum aestivum
ubiquitin activating enzyme. E1.

CAA71762.1 Y10804 Nicotiana tabacum
Ubiquitin activating enzyme E1. UBA1.

SEQ ID NO: 929

CAA55693.1 X79086 Zea mays
initiator-binding protein. IBP2.

CAC19789.1 AJ251686 Catharanthus roseus
putative transcription factor. MYB-like DNA-binding protein. bpf-1.

CAA55691.1 X79085 Zea mays
initiator binding protein. IBP1.

AAF97508.1 AF242298 Oryza sativa
telomere binding protein-1. TBP1.

SEQ ID NO: 930

AAK15447.1 AC037426 Oryza sativa
putative flavin-containing monooxygenase. OSJNBb0014I11.12.

AAK15439.1 AC037426 Oryza sativa
putative flavin-containing monooxygenase. OSJNBb0014I11.8.

BAA88198.1 AP000837 Oryza sativa
Similar to human dimethylaniline monooxygenase (AC002376).

BAA88195.1 AP000837 Oryza sativa
Similar to human dimethylaniline monooxygenase (AC002376).

BAB32703.1 AP002902 Oryza sativa
dimethylaniline monooxygenase-like protein. P0492F05.5. contains EST C72123(E1029).

BAB07916.2 AP002835 Oryza sativa
dimethylaniline monooxygenase-like protein. P0417G05.24. contains EST C72123(E1029).

SEQ ID NO: 931

AAG38521.1 AF283536 Citrus x paradisi
cystatin-like protein. cystein proteinase inhibitor.

AAA97905.1 U51853 Glycine max
cysteine proteinase inhibitor.

CAA79954.1 Z21954 Vigna unguiculata
cysteine proteinase inhibitor.

AAB66355.1 U54702 Oryza sativa
thiol proteinase inhibitor; cysteine proteinase inhibitor. oryzacystatin. has potential for insect resistance in rice and for cancer therapeutics.

AAB24010.1 S49967 Oryza
oryzacystatin. oryzacystatin. cysteine protease inhibitor; This sequence comes from Fig. 1.

CAA60610.1 X87126 Zea mays
cysteine proteinase inhibitor. zmc-II.

BAA09666.1 D63342 Zea mays
cysteine proteinase inhibitor. gCC.

AAA32672.1 L16624 Ambrosia artemisiifolia
cystatin proteinase inhibitor.

BAA07327.1 D38130 Zea mays
inhibition against cysteine proteinases. cystatin II.

AAA97907.1 U51855 Glycine max
cysteine proteinase inhibitor.

BAB18766.1 AB038392 Triticum aestivum
cysteine proteinase inhibitor. WC61. cystatin.

BAB18767.1 AB038393 Triticum aestivum
cysteine proteinase inhibitor. WC92. cystatin.

CAA11899.1 AJ224331 Castanea sativa
cysteine proteinase inhibitor. cystatin.

AAB71505.1 U82220 Pyrus communis
cysteine protease inhibitor.

AAA79239.1 L48182 Brassica rapa
cysteine proteinase inhibitor. N-terminal deletion clone; putative.

CAA60634.1 X87168 Sorghum bicolor
cysteine proteinase inhibitor. CPI1.

AAA68150.1 L42819 Brassica rapa
cysteine proteinase inhibitor. N-terminal deletion clone; putative.

BAB18765.1 AB038391 Triticum aestivum
cysteine proteinase inhibitor. gWC2. cystatin.

BAB18768.1 AB038394 Triticum aestivum
cysteine proteinase inhibitor. WC83. cystatin.

AAC37479.1	L41355	Brassica rapa cysteine proteinase inhibitor.
BAA28867.1	AB014760	Cucumis sativus root-specific cystein protease inhibitor. cystein proteinase inhibitor.
AAD33907.1	AF143677	Artemisia vulgaris cysteine proteinase inhibitor. CPI. pollen cystatin.
BAA89582.1	AP001073	Oryza sativa ESTs AU067919(C10906),AU067918(C10906) correspond to a region of the predicted gene. Similar to cysteine proteinase inhibitor (D31700).
CAA72790.1	Y12068	Hordeum vulgare cysteine proteinase inhibitor. CPI.
AAA96316.1	U51119	Brassica rapa cysteine proteinase inhibitor. BCPI-2.
AAK15090.1	AF240007	Sesamum indicum cystatin. cysteine proteinase inhibitor.
AAF23127.1	AF198389	Lycopersicon esculentum cysteine proteinase inhibitor. cystatin. STC. expression induced by arachidonic acid and gamma linolenic acid.
BAA19610.1	D64115	Glycine max cysteine proteinase inhibitor. cystatin.
BAA19608.1	D31700	Glycine max cysteine proteinase inhibitor. cystatin.
CAA89697.1	Z49697	Ricinus communis cysteine proteinase inhibitor.
AAF72202.1	AF265551	Manihot esculenta cysteine protease inhibitor.
AAA97906.1	U51854	Glycine max cysteine proteinase inhibitor.
CAA50437.1	X71124	Carica papaya cysteine proteinase inhibitor (cystatin).
AAF23126.1	AF198388	Lycopersicon esculentum cysteine proteinase inhibitor. cystatin. LTC. expression induced by arachidonic acid and gamma linolenic acid.
AAD13812.1	AF117334	Ipomoea batatas cysteine proteinase inhibitor. cystatin.
AAF64480.1	AF241536	Ipomoea batatas cysteine protease inhibitor. CYSPI.
AAK30004.1	AY028994	Dianthus caryophyllus cysteine proteinase inhibitor. DC-CPIn.
BAB18769.1	AB038395	Triticum aestivum cysteine proteinase inhibitor. WC81. cystatin.
AAC32853.1	AF083253	Lycopersicon esculentum cysteine protease inhibitor.

SEQ ID NO: 938

CAA06486.1 AJ005340 *Linum usitatissimum*
IAA amidohydrolase. homolog.

SEQ ID NO: 940

BAB17350.1 AP002747 *Oryza sativa*
putative nodulin. P0698G03.34. contains ESTs
D39891(S1543),D41717(S4395),AU033037(S1543).

BAA85440.1 AP000616 *Oryza sativa*
ESTs AU055729(S20023),AU055730(S20023) correspond to a region of the predicted gene.;
similar to *Medicago nodulin N21*-like protein (AC004218).

CAB53493.1 AJ245900 *Oryza sativa*
CAA303720.1 protein. q3037.20. Similar to *Medicago nodulin N21* (MtN21).

SEQ ID NO: 941

BAA21921.1 AB006599 *Petunia x hybrida*
ZPT2-12. C2H2 zinc finger protein, 2 finger.

BAA21922.1 AB006600 *Petunia x hybrida*
ZPT2-13. C2H2 zinc finger protein, 2finger.

BAA19110.1 AB000451 *Petunia x hybrida*
PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA21923.1 AB006601 *Petunia x hybrida*
ZPT2-14. C2H2 zinc finger protein, 2 finger.

BAA21925.1 AB006603 *Petunia x hybrida*
ZPT2-8. C2H2 zinc finger protein, 2 finger.

BAA21924.1 AB006602 *Petunia x hybrida*
ZPT2-7. C2H2 zinc finger protein, 2finger.

BAA21920.1 AB006598 *Petunia x hybrida*
ZPT2-11. C2H2 zinc finger protein, 2finger.

CAA60828.1 X87374 *Pisum sativum*
putative zinc finger protein.

BAA19111.1 AB000452 *Petunia x hybrida*
PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA21926.1 AB006604 *Petunia x hybrida*
ZPT2-9. C2H2 zinc finger protein, 2 finger.

BAA21927.1 AB006605 *Petunia x hybrida*
ZPT3-3. C2H2 zinc finger protein, 3 finger.

BAA96071.1 AB035133 *Petunia x hybrida*
C2H2 zinc-finger protein ZPT3-3. ZPT3-3.

BAA21919.1 AB006597 *Petunia x hybrida*
ZPT2-10. C2H2 zinc finger protein, 2 finger.

BAA96070.1 AB035132 *Petunia x hybrida*
C2H2 zinc-finger protein ZPT2-10. PETHy;ZPT2-10.

CAB77055.1 Y18788 *Medicago sativa*
putative TFIIIA (or kruppel)-like zinc finger protein.

AAB53260.1	U76554	Brassica rapa transcription factor. zinc-finger protein-1. BR42.
AAB53261.1	U76555	Brassica rapa zinc-finger protein BcZFP1. BcZFP1(3-2z).
BAA19114.1	AB000455	Petunia x hybrida PEThy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.
BAA05078.1	D26085	Petunia x hybrida zinc-finger DNA binding protein.
AAD26942.1	AF119050	Datisca glomerata zinc-finger protein 1. zfp1. DgZFP1.
BAA05077.1	D26084	Petunia x hybrida zinc-finger DNA binding protein.
AAB39638.1	U68763	Glycine max putative transcription factor. SCOF-1. scof-1. zinc-finger protein.
AAC06243.1	AF053077	Nicotiana tabacum transcription factor. osmotic stress-induced zinc-finger protein. zfp.
BAA19112.1	AB000453	Petunia x hybrida PEThy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.
AAK01713.1	AF332876	Oryza sativa zinc finger transcription factor ZF1.
BAA05076.1	D26083	Petunia x hybrida zinc-finger DNA binding protein.
BAA05079.1	D26086	Petunia x hybrida zinc-finger protein.
BAA21928.1	AB006606	Petunia x hybrida ZPT4-4. C2H2 zinc finger protein, 4 finger.
BAA19926.1	AB000456	Petunia x hybrida PEThy; ZPT4-2. C2H2 zinc finger protein, 4 finger.
BAA19113.1	AB000454	Petunia x hybrida PEThy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.
SEQ ID NO: 945		
AAG10793.1	AF296158	Citrus unshiu beta-carotene hydroxylase. CHX1.
AAG33636.1	AF315289	Citrus unshiu beta-carotene hydroxylase. CHX2. similar to beta-carotene hydroxylase of Citrus unshiu encoded by GenBank Accession Number AF296158.
AAG10430.1	AF251018	Tagetes erecta beta hydroxylase.
CAB55625.1	Y14809	Lycopersicon esculentum beta-carotene hydroxylase. CrtR-b1.
CAA70888.1	Y09722	Capsicum annuum beta-carotene hydroxylase 2.

CAB55626.1 Y14810 *Lycopersicon esculentum*
beta-carotene hydroxylase. CrtR-b2.

CAA70427.1 Y09225 *Capsicum annuum*
beta-carotene hydrolase.

CAC06712.1 AJ278882 *Narcissus pseudonarcissus*
synthesis of zeaxanthin. beta-carotene hydroxylase.

AAD54243.1 AF162276 *Haematococcus pluvialis*
carotenoid hydroxylase.

SEQ ID NO: 946

AAC18914.1 U94748 *Petunia x hybrida*

AN11. An11. No functional information available. Protein is involved in transcriptional regulation of anthocyanin biosynthesis in petunia. Protein contains five WD 40 repeats; WD 40 repeat protein.

SEQ ID NO: 948

AAG52887.1 AF333386 *Nicotiana tabacum*
beta-expansin-like protein. PPAL. pollen allergen-like protein.

AAF72986.1 AF261273 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB5.

AAF72990.1 AF261277 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB9. putative group-1 pollen allergen.

BAB20817.1 AB051899 *Atriplex lentiformis*
beta-expansin. Al-EXP1.

AAF72984.1 AF261271 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB3.

AAK15453.1 AC037426 *Oryza sativa*
beta-expansin EXPB3. OSJNBb0014I11.1.

AAF72991.1 AF261278 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB10. putative group-1 pollen allergen.

AAK15442.1 AC037426 *Oryza sativa*
beta-expansin EXPB6. OSJNBb0014I11.3.

AAF72987.1 AF261274 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB6.

AAF72983.1 AF261270 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB1. putative group-1 pollen allergen Ory s1.

AAF72988.1 AF261275 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB7.

AAF72989.2 AF261276 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB8.

AAF72985.1 AF261272 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB4.

AAK15440.1	AC037426	Oryza sativa beta-expansin EXPB2. OSJNBb0014I11.2.
AAB61710.1	U95968	Oryza sativa beta-expansin. EXPB2. cell wall loosening protein.
AAB37749.1	U30460	Cucumis sativus expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAD38296.1	AC007789	Oryza sativa putative expansin. OSJNBa0049B20.23.
BAB18336.1	AP002865	Oryza sativa putative expansin. P0034C11.27.
CAC19183.1	AJ291816	Cicer arietinum expansin.
AAG13983.1	AF297522	Prunus avium expansin 2. Exp2. PruavExp2.
AAG01875.1	AF291659	Striga asiatica alpha-expansin 3. Exp3.
AAG32920.1	AF184232	Lycopersicon esculentum expansin. Exp8.
AAC96077.1	AF049350	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
AAC96078.1	AF049351	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
AAF35902.1	AF230333	Zinnia elegans expansin 3.
BAA88200.1	AP000837	Oryza sativa EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAC39512.1	AF043284	Gossypium hirsutum expansin. GhEX1. contains N-terminal signal peptide.
AAD38297.1	AC007789	Oryza sativa putative expansin. OSJNBa0049B20.24.
AAF32411.1	AF230278	Triphysaria versicolor alpha-expansin 1.
BAB18338.1	AP002865	Oryza sativa putative expansin. P0034C11.29.
AAG32921.1	AF184233	Lycopersicon esculentum expansin. Exp10.
CAC19184.1	AJ291817	Cicer arietinum expansin.
AAC96079.1	AF049352	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.

SEQ ID NO: 950

CAA52213.1	X74115	Picea abies short-chain alcohol dehydrogenase.
AAC35342.1	AF072449	Ipomoea trifida short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAC35340.1	AF072447	Ipomoea trifida short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
CAA11153.1	AJ223177	Nicotiana tabacum short chain alcohol dehydrogenase.
CAA11154.1	AJ223178	Nicotiana tabacum short chain alcohol dehydrogenase. SCANT.
AAK29646.1	AF349916	Solanum tuberosum putative short-chain type alcohol dehydrogenase. GAN; similar to tomato Leert10 and maize Ts2.
AAC37345.1	L20621	Zea mays alcohol dehydrogenase. short chain.
AAC35341.1	AF072448	Ipomoea trifida short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAC35343.1	AF072450	Ipomoea trifida short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAB57737.1	U89270	Tripsacum dactyloides short-chain alcohol dehydrogenase. gynomonoecious sex form 1. similar to Zea mays tasselseed 2: SwissProt Accession Number P50160.
AAF89645.1	AF169018	Glycine max seed maturation protein PM34. PM34. similar to bacterial glucose and ribitol dehydrogenase.
AAF04253.1	AF097651	Pisum sativum short-chain alcohol dehydrogenase SAD-C. sadC. contains the entire nucleotide binding motif of 3(alpha), 20(beta)-hydroxysteroid dehydrogenases, GXXXXXXGXXG(A)XGXXXA (Ghosh et al., 1991, Proc. Natl. Acad. Sci. USA 88, 10064-10068).
AAF04193.1	AF053638	Pisum sativum short-chain alcohol dehydrogenase. sadA. contains the entire nucleotide binding motif of the 3(alfa),20(beta)-hydroxysteroid dehydrogenase: GXXXXXXGXXG(A)XGXXXA (Ghosh et al. (1991) Proc. Natl. Acad. Sci. USA 88, 10064-10068); similar to Lycopersicon esculentum product encoded by GenBank Accession Number U21801 and Streptomyces hydrogenans steroid alcohol dehydrogenase.
AAB57738.1	U89271	Tripsacum dactyloides short-chain alcohol dehydrogenase. gynomonoecious sex form 1. similar to Zea mays tasselseed 2: SwissProt Accession Number P50160.
CAB91875.1	AJ277945	Lycopersicon esculentum putative alcohol dehydrogenase. yfe37.
AAF04194.1	AF053639	Pisum sativum short-chain alcohol dehydrogenase. sadB. contains the Prosite pattern no. PS00061 for short-chain alcohol dehydrogenases; contains a deletion in the nucleotide binding motif of the 3(alfa),20(beta)-hydroxysteroid dehydrogenase: GXXXXXXGXXG(A)XGXXXA (Ghosh et al. (1991) Proc. Natl. Acad. Sci. USA 88, 10064-10068).

AAB00109.1	U21801	<i>Lycopersicon esculentum</i> alcohol dehydrogenase homolog. GAD3. mRNA is suppressed in the presence of gibberellin; similar to nonmetallo-short-chain alcohol dehydrogenases, PIR Accession Number A47542.
SEQ ID NO: 952		
CAB63264.1	AJ251808	<i>Lotus japonicus</i> calcium-binding protein. cbp1.
AAG43547.1	AF211529	<i>Nicotiana tabacum</i> Avr9/Cf-9 rapidly elicited protein 31. ACRE31. similar to Solanum tuberosum CAST calcium binding protein encoded by GenBank Accession Number L02830.
AAA34014.1	L01432	<i>Glycine max</i> calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAA34013.1	L01430	<i>Glycine max</i> calcium-binding regulatory protein. calmodulin. SCaM-1. putative.
AAA92681.1	U13882	<i>Pisum sativum</i> calcium-binding protein. calmodulin.
CAA78301.1	Z12839	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin. putative.
AAA19571.1	U10150	<i>Brassica napus</i> calcium binding. calmodulin. bcm1.
AAA85157.1	U20297	<i>Solanum tuberosum</i> calcium-binding protein. calmodulin.
AAA85156.1	U20296	<i>Solanum tuberosum</i> calcium-binding protein. calmodulin.
AAA62351.1	U20295	<i>Solanum tuberosum</i> calcium-binding protein. calmodulin.
AAA85155.1	U20294	<i>Solanum tuberosum</i> calcium-binding protein. calmodulin.
AAC49587.1	U49105	<i>Triticum aestivum</i> calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	<i>Triticum aestivum</i> calmodulin TaCaM3-3. calcium-binding protein.
AAC49585.1	U49103	<i>Triticum aestivum</i> calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	<i>Triticum aestivum</i> calmodulin TaCaM3-1. calcium-binding protein.
AAC49580.1	U48689	<i>Triticum aestivum</i> calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	<i>Triticum aestivum</i> calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	<i>Triticum aestivum</i> calmodulin TaCaM1-1. calcium-binding.

CAA78287.1 Z12827 Oryza sativa
calcium binding protein, signal transduction. calmodulin.

AAA03580.1 L01431 Glycine max
calcium-binding regulatory protein. calmodulin. SCaM-2. putative.

AAA33901.1 L18913 Oryza sativa
calcium binding protein, signal transduction. calmodulin. putative.

AAA34015.1 L01433 Glycine max
calcium-binding regulatory protein. calmodulin. SCaM-4. putative.

Table 24 Plant Open Reading Frames (ORFs) orthologous to specific *Chenopodium* ORFs

SEQ ID NO:1956
CAB51903.1 AJ242807 <i>Brassica napus</i> endo-1,4-beta-D-glucanase. Cel16. cellulase.
BAA94257.1 AB040769 <i>Hordeum vulgare</i> endo-1,4-beta-glucanase Cel1. Cel1.
AAC49704.1 U78526 <i>Lycopersicon esculentum</i> endo-1,4-beta-glucanase. Cel3.
SEQ ID NO:1957
BAB21273.1 AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.4.
BAB21275.1 AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.6.
BAB21276.1 AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
CAA94437.1 Z70524 <i>Spirodela polyrrhiza</i> multidrug resistance protein. PDR5-like ABC transporter.
BAB21279.1 AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463), AU101680(R3463).
CAA03960.1 AJ000234 <i>Hordeum vulgare</i> partial sequence, homology to PDR5-like ABC transporter.
SEQ ID NO:1960
AAD51778.1 AF116858 <i>Phaseolus vulgaris</i> utilizes UDPX as the sugar donor and catalyzes the formation of O-xylosylzeatin from zeatin. zeatin O-xylosyltransferase. ZOX1.
AAD04166.1 AF101972 <i>Phaseolus lunatus</i> catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
BAA36410.1 AB012114 <i>Vigna mungo</i> UDP-glycoside:flavonoid glycosyltransferase. UFGlyT.
BAB17061.1 AP002523 <i>Oryza sativa</i> putative glucosyl transferase. P0013F10.7. contains EST C73149(E2992).

BAA36412.1 AB012116 *Vigna mungo*

UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

AAK28303.1 AF346431 *Nicotiana tabacum*

phenylpropanoid:glucosyltransferase 1. tog1.
glucosyltransferase.

BAB17059.1 AP002523 *Oryza sativa*

putative glucosyl transferase. P0013F10.5.

AAF17551.1 AF198453 *Glycine max*

UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

AAB36653.1 U32644 *Nicotiana tabacum*

immediate-early salicylate-induced glucosyltransferase.

IS5a.

CAB88666.1 AJ400861 *Cicer arietinum*

flavonoid glycosyltransferase. putative UDP-glycose.

AAB36652.1 U32643 *Nicotiana tabacum*

immediate-early salicylate-induced glucosyltransferase.

IS10a.

CAA54612.1 X77462 *Manihot esculenta*

UTP-glucose glucosyltransferase. CGT5.

BAB17060.1 AP002523 *Oryza sativa*

putative glucosyl transferase. P0013F10.6.

AAK28304.1 AF346432 *Nicotiana tabacum*

phenylpropanoid:glucosyltransferase 2. tog2.
glucosyltransferase.

CAA59450.1 X85138 *Lycopersicon esculentum*

tw1. homologous to glucosyltransferases.

BAA83484.1 AB031274 *Scutellaria baicalensis*

UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

CAA54611.1 X77461 *Manihot esculenta*

UTP-glucose glucosyltransferase. CGT2.

BAA36411.1 AB012115 *Vigna mungo*

UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

CAC35167.1 AJ310148 *Rauvolfia serpentina*

arbutin synthase. as.

BAB17182.1 AP002843 *Oryza sativa*

putative UTP-glucose glucosyltransferase. P0407B12.19.

CAB56231.1 Y18871 *Dorotheanthus bellidiformis*
betanidin-5-O-glucosyltransferase.

BAB17176.1 AP002843*Oryza sativa*
putative UTP-glucose glucosyltransferase. P0407B12.13.

AAK16172.1 AC079887*Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.14.

CAA54613.1 X77463 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT6.

AAF61647.1 AF190634*Nicotiana tabacum*
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA93039.1 AB033758*Citrus unshiu*
limonoid UDP-glucosyltransferase. LGTase.

CAA54610.1 X77460 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT4.

AAA59054.1 L34847 *Zea mays*
conjugation of the growth hormone indole-3-acetic acid
(IAA). IAA-glu synthetase. iaglu.

BAA36423.1 AB013598*Verbena x hybrida*
UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

AAF17077.1 AF199453*Sorghum bicolor*
UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.

CAA54558.1 X77369 *Solanum melongena*
glycosyl transferase. GT.

AAK16175.1 AC079887*Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.15.

CAA81057.1 Z25802 *Petunia x hybrida*
UDP rhamnose: anthocyanidin-3-glucoside
rhamnosyltransferase.

CAA50377.1 X71060 *Petunia x hybrida*
anthocyanin: rhamnosyltransferase. rt.

CAA50376.1 X71059 *Petunia x hybrida*
anthocyanin 3 glucoside: rhamnosyltransferase. rt.

AAK16181.1 AC079887*Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.16.

AAK16178.1 AC079887*Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.5.

AAD21086.1 AF127218Forsythia x intermedia
adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.

BAA89008.1 AB027454Petunia x hybrida
anthocyanidin 3-O-glucosyltransferase. PGT8.

SEQ ID NO:1962

CAA65580.1 X96784 Nicotiana tabacum
cytochrome P450. hsr515.

CAA64635.1 X95342 Nicotiana tabacum
cytochrome P450. hsr515. hypersensitivity-related gene.

AAG44132.1 AF218296Pisum sativum
cytochrome P450. P450 isolog.

AAG49299.1 AF313489Callistephus chinensis
flavonoid 3',5'-hydroxylase.

BAA03438.1 D14588 Petunia x hybrida
flavonoid-3',5'-hydroxylase. Hf1.

AAC32274.1 AF081575Petunia x hybrida
flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.

CAA50442.1 X71130 Petunia x hybrida
P450 hydroxylase. PET 1.

CAA80266.1 Z22545 Petunia x hybrida
flavonoid 3',5'-hydroxylase.

AAG49315.1 AF315465Pelargonium x hortorum
flavonoid 3'-hydroxylase.

AAG49298.1 AF313488Callistephus chinensis
putative flavonoid 3'-hydroxylase.

AAB17562.1 U72654 Eustoma grandiflorum
flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.

BAB20076.1 AB012925Torenia hybrida
flavonoid 3',5'-hydroxylase. F3'5'H.

AAG14961.1 AF214007Brassica napus
cytochrome p450-dependent monooxygenase. BNF5H1.

CAC26920.1 AJ295586Arabidopsis lyrata subsp. petraea
ferulate-5-hydroxylase. fah1.

AAG14962.1 AF214008Brassica napus
cytochrome p450-dependent monooxygenase. BNF5H2.

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15 All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied
20 considerably without departing from the basic principles of the invention.

WHAT IS CLAIMED IS:

1. A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen comprising:
 - 5 a) determining or detecting plant gene expression in an incompatible interaction; and
 - b) identifying at least one gene whose expression is significantly altered in the incompatible interaction relative to expression of the at least one gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to infection by a pathogen, or in a corresponding compatible interaction.
- 10 2. A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen comprising:
 - a) determining or detecting plant gene expression in a compatible interaction; and
 - b) identifying at least one gene whose expression is significantly altered in the compatible interaction relative to expression of the at least one gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to infection by a pathogen, or in a corresponding incompatible interaction.
- 15 3. The method of claim 1 or 2 wherein the compatible interaction is between a plant having a resistance gene and a pathogen lacking a corresponding avirulence gene, a plant lacking a resistance gene to a pathogen having a corresponding avirulence gene, or a plant lacking a resistance gene and a pathogen lacking a corresponding avirulence gene.
- 20 4. The method of claim 1 or 2 wherein expression of the at least one gene is upregulated in response to infection.
- 25 5. The method of claim 1 or 2 wherein expression of the at least one gene is downregulated in response to infection.
- 30 6. The method of claim 1 or 2 wherein the at least one gene encodes a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.

7. The method of claim 1 or 2 wherein the at least one gene comprises an open reading frame comprising one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.
8. The method of claim 1 or 2 wherein the pathogen is a bacterium.
5
9. The method of claim 1 or 2 wherein the pathogen is a fungus.
10. The method of claim 1 or 2 wherein the pathogen is a virus.
- 10 11. The method of claim 1 or 2 wherein gene expression is detected or determined using a gene chip, a cDNA array, cDNA-AFLP, or differential display PCR
12. The method of any one of claims 1 to 6 or 8 to 11 wherein the plant is a dicot.
- 15 13. The method of any one of claims 1 to 6 or 8 to 11 wherein the plant is a monocot.
14. The method of any one of claims 1 to 13 further comprising isolating the at least one gene or a portion thereof which includes the open reading frame or promoter for the gene.
- 20 15. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation that decreases jasmonic acid or ethylene-dependent signaling, comprising:
 - a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
 - b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having the mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.
- 25
- 30

16. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation in a gene that interferes with salicylic acid dependent signaling, comprising:

5 a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and

10 b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having a mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.

15 17. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation that results in enhanced susceptibility to bacterial infection, comprising:

20 a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and

25 b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having a mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.

30 18. A method to identify at least one gene, the expression of which is altered by infection with at least one virus, comprising:

 a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with a virus, so as to form a

complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and

5 b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from an uninfected plant, so as to identify a gene, the expression of which is altered by virus infection.

19. A method to identify at least one gene, the expression of which is altered by infection with at least one pathogen comprising:

10 a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from an incompatible interaction so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and

15 b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from a corresponding compatible interaction so as to identify a gene, the expression of which is altered by the pathogen.

20 20. The method of any one of claims 15 to 19 wherein the at least one gene is upregulated.

21. The method of any one of claims 15 to 19 wherein the at least one gene is downregulated.

25 22. The method of any one of claims 15 to 19 wherein the gene which is identified encodes a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising any one of SEQ ID NOS:1-953, 1954-1966, 2000-2129 or 2662-4737.

30 23. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from a dicot.

24. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from a cereal plant.

25. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from
a monocot.

26. The method of any one of claims 15 to 19 further comprising identifying the promoter for
5 the at least one gene.

27. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription
of an operatively linked nucleic acid segment in a plant cell after pathogen infection,
which plant nucleotide sequence is from a gene encoding a polypeptide that is
10 substantially similar to a polypeptide encoded by a gene comprising a promoter selected
from the group consisting of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.

28. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription
of an operatively linked nucleic acid segment in a plant cell after pathogen infection,
15 which plant nucleotide sequence hybridizes under high stringency conditions to the
complement of any one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.

29. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription
of an operatively linked nucleic acid segment in a plant after pathogen infection, which
20 plant nucleotide sequence hybridizes under very high stringency conditions to the
complement of any one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.

30. An isolated polynucleotide comprising a plant nucleotide sequence that directs
transcription of an operatively linked nucleic acid segment in a plant cell, which plant
25 nucleotide sequence is selected from the group consisting of SEQ ID NOs:2137-2661 and
or SEQ ID NOs:4738-6813.

31. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence is
25 to 2000 nucleotides in length.

30
32. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence
has at least 90% nucleotide sequence identity to one of SEQ ID NOs:2137-2661 or SEQ
ID NOs:4738-6813.

33. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence has at least 98% nucleotide sequence identity to one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.

5

34. The polynucleotide of any one of claims 27 to 29 and 31 to 33 wherein the plant nucleotide sequence is from a dicot.

10

35. The polynucleotide of any one of claims 26 to 29 and 31 to 33 wherein the plant nucleotide sequence is from a monocot.

15

36. The polynucleotide of any one of claims 26 to 29 and 31 to 33 wherein the plant nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.

20

37. The polynucleotide of any one of claims 27 to 36 which comprises a TATA box, a CAAT box, or both.

38. A composition comprising the polynucleotide of any one of claims 27 to 37.

25

39. A recombinant vector comprising the polynucleotide of any one of claims 27 to 38.

40. The vector of claim 39 which is selected from the group consisting of a plasmid, phagemid, cosmid, virus, F-factor and phage.

25

41. An expression cassette comprising the polynucleotide of any one of claims 27 to 37 operatively linked to an open reading frame.

42. The expression cassette of claim 41 operably linked to other suitable regulatory sequences.

30

43. The expression cassette of claim 41 wherein the open reading frame is in an antisense orientation relative to the nucleotide sequence which alters transcription.

44. The expression cassette of claim 41 wherein the open reading frame is in a sense orientation relative to the nucleotide sequence which alters transcription.

45. A recombinant vector comprising the expression cassette of claim 41.

5

46. The vector of claim 45 wherein the vector is selected from the group consisting of a plasmid, phagemid, cosmid, virus, F-factor or phage.

47. A host cell comprising the expression cassette of claim 41.

10

48. The host cell of claim 47 wherein the cell is selected from the group consisting of a yeast, a bacterium, a cereal plant cell, and an *Arabidopsis* cell.

49. A plant cell containing the expression cassette of claim 41.

15

50. The plant cell of claim 49 which is a monocot cell.

51. The plant cell of claim 49 which is a dicot cell.

20 52. A transformed plant, the genome of which is augmented with the expression cassette of claim 41.

53. A transformed plant comprising transformed plant cells, which cells contain the expression cassette of claim 41.

25

54. The transformed plant of claim 52 or 53 which is a dicot.

55. The transformed plant of claim 52 or 53 which is a monocot.

30 56. The transformed plant of claim 52 or 53 which is selected from the group consisting of maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat and *Arabidopsis*.

57. A method for augmenting a plant genome, comprising:

- contacting plant cells with the expression cassette of claim 41 so as to yield a transformed plant cell; and
- regenerating the transformed plant cell to provide a differentiated transformed plant,
5 wherein the differentiated transformed plant expresses the open reading frame in the cells of the plant.

58. A method to alter the phenotype of a plant cell comprising: introducing the expression cassette of claim 41 into a plant cell and expressing that open reading frame in the cell so
10 as to alter a characteristic of that cell relative to a plant cell that does not comprise the expression cassette.

59. The method of claim 57 or 58 wherein the plant cell is a dicot cell.

15 60. The method of claim 57 or 58 wherein the plant is a monocot cell.

61. The method of claim 57 or 58 wherein the plant cell a cereal cell.

62. The method of claim 57 or 58 wherein the plant cell is selected from the group consisting
20 of a cell of maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat and *Arabidopsis*.

63. The method of claim 57 or 58 wherein the open reading frame is in an antisense orientation relative to the nucleotide sequence which alters transcription.
25

64. The method of claim 57 or 58 wherein the expression inhibits transcription or translation of endogenous plant nucleic acid sequences corresponding to the open reading frame.

65. The method of claim 57 or 58 wherein the open reading frame is in a sense orientation
30 relative to the nucleotide sequence which alters transcription.

66. The method of claim 57 wherein the open reading frame is expressed in an amount that is greater than the amount in a plant which does not comprise the expression cassette.

67. The method of claim 57 or 58 wherein the open reading frame encodes a protein.

68. The method of claim 67 wherein the protein encodes a regulatory product.

5

69. The method of claim 67 wherein the expression of the open reading frame confers insect resistance, bacterial resistance, fungal resistance, viral resistance, or nematode resistance.

70. A transformed plant prepared by the method of claim 57.

10

71. A product of the plant of claim 70 which comprises the expression cassette or the gene product encoded by the open reading frame.

15

72. The product of claim 71 which is selected from the group consisting of a seed, fruit, vegetable, transgenic plant, and a progeny plant.

73. A computer-readable medium having stored thereon a data structure comprising:

20

- a) a nucleic acid molecule that has at least 70% nucleic acid sequence identity to a nucleotide molecule selected from the group consisting of SEQ ID NOs:1-953, 2137-2661, 1954-1966, 2000-2129, 2662-4737, 4738-6813 or the complement thereof; and
- b) a module receiving the nucleic acid molecule which compares the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

25

74. The computer readable medium of claim 73 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.

75. A computer-readable medium having stored thereon computer executable instructions for performing a method comprising:

30

- a) receiving a nucleic acid molecule having at least 70% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-953, 2137-2661, 1954-1966, 2000-2129, 2662-4737, 4738-6813 or the complement thereof; and

- b) comparing the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

76. The computer readable medium of claim 75 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.

77. The computer readable medium of any one of claims 73 to 76 wherein the nucleotide sequence is not SEQ ID NOs. 1-208, 210-215, 217-261, 263-266, 268-316, 318-385, 387-424, 426-439, 441-799, or 801-953.

78. A method to confer resistance or tolerance to a plant to a pathogen, comprising:

- a) contacting plant cells with an expression cassette comprising a polynucleotide encoding a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 so as to yield transformed cells; and
- b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the polynucleotide in the cells of the plant in an amount effective to confer resistance or tolerance to the plant to a pathogen relative to a corresponding plant which does not comprise the expression cassette.

79. The method of claim 78 wherein the polynucleotide hybridizes under moderate stringency conditions to the complement of any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.

80. The method of any one of claims 78 to 79 wherein the cells are monocot cells.

81. The method of any one of claims 78 to 79 wherein the cells are dicot cells.

82. The method of claim 78 wherein the open reading frame encodes a DNA binding protein, hormone response protein, membrane protein, metabolic protein, transposon, receptor/kinase, phosphatase, stress protein, cell wall protein, lipid transfer protein, heat

shock protein, protein processing protein, RNA processing protein, non-cell wall structural protein or a non-kinase signaling protein.

83. A transformed plant prepared by the method of any one of claims 78 to 82.

5

84. A seed of the plant of claim 83.

85. A progeny plant of the plant of claim 83.

10 86. A method to identify a plant cell infected with a pathogen, comprising:

- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with at least one oligonucleotide under conditions effective to specifically amplify a nucleotide sequence corresponding to one of SEQ ID NOS:1-953, 1954-1966, 2000-2129 or 2662-4737 or a portion thereof, so as to yield an amplified product; and
- b) detecting or determining the presence or amount of the amplified product, wherein the presence or amount of the amplified product is indicative of pathogen infection.

87. A method to identify a plant cell infected with a pathogen, comprising:

- a) contacting a sample comprising polypeptides obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds to a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising one of SEQ ID NOS:1-953, 1954-1966, 2000-2129 or 2662-4737 so as to form a complex, wherein the; and
- b) detecting or determining the presence or amount of the complex, wherein the presence or amount of the complex is indicative of pathogen infection.

88. A method to identify a plant cell infected with a pathogen, comprising:

- a) contacting nucleic acid obtained from a plant cell suspected of being infected with a pathogen with a probe corresponding to a sequence selected from the group consisting of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737 or a portion thereof, under stringent hybridization conditions to form a duplex, and

b) detecting or determining the presence or amount of the duplex, wherein the presence of a duplex is indicative of infection.

89. A method for marker-assisted breeding to select for plants having altered
5 resistance to a pathogen comprising:

a) contacting plant DNA or cDNA with a probe comprising a sequence selected from the group consisting of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737 or a portion thereof which hybridizes under moderate stringency conditions to a gene corresponding to one of of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737
10 so as to form a duplex; and

b) detecting or determining the presence or amount of the duplex, wherein the amount or presence of the duplex is indicative of the presence of a gene, the expression of which alters the resistance of the plant to a pathogen.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 01/01105

A. CLASSIFICATION OF SUBJECT MATTER		
IPC 7 C12N15/29 C12N15/82 C12Q1/68 A01H5/00 G06F17/00 C07K14/415		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 7 C07K C12N		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practical, search terms used) EPO-Internal, WPI Data, PAJ, BIOSIS, MEDLINE, SEQUENCE SEARCH		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SCHENK P M ET AL: "Coordinated plant defense responses in <i>Arabidopsis</i> revealed by microarray analysis" <i>PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE</i> . WASHINGTON, US, vol. 97, no. 21, 10 October 2000 (2000-10-10), pages 11655-11660, XP002153163 ISSN: 0027-8424 the whole document --- WO 97 49822 A (CIBA GEIGY AG ; ELLIS DANIEL MURRAY (US); FRIEDRICH LESLIE BETHARDS) 31 December 1997 (1997-12-31) the whole document --- -/--	1-5, 8-21, 23-26
X		1-5, 8-21, 23-26
<input checked="" type="checkbox"/> Further documents are listed in the continuation of box C.		<input checked="" type="checkbox"/> Patent family members are listed in annex.
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the International filing date "L" document which may throw doubts on priority, claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the International filing date but later than the priority date claimed		
"T" later document published after the International filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "&" document member of the same patent family		
Date of the actual completion of the International search 9 July 2002	Date of mailing of the International search report 25.09.2002	
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 esp nl, Fax: (+31-70) 340-3016	Authorized officer Oderwald, H	

INTERNATIONAL SEARCH REPORT

International Application No PCT/IB 01/01105

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01 07603 A (TUZUN SADIK ;UNIV AUBURN (US); ABDULLAH MALIKAH (US); SINGH NAREND) 1 February 2001 (2001-02-01) the whole document ---	1-5, 8-21, 23-26
X	EP 1 033 405 A (CERES INC) 6 September 2000 (2000-09-06)	73-76, 78-86, 88,89
A	page 1 -page 26 see SEQ IN NO: 38097 page 325 -page 341; claims 1-34 -----	6,7,22

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 01/01105

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: 87 because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of Invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple Inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
Claims 1-26, 73-89 partially.

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 87

Present claim 87 relates to a product/compound defined by reference to a desirable characteristic or property, namely an agent that binds to a polypeptide encoded by an open reading frame.

The claims cover all products/compounds having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such products/compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the product/compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, no search has been carried out.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-26, 73-89 partially

A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen wherein the gene encodes a polypeptide encoded by an open reading frame comprising SEQ ID NO: 1. A method to identify at least one gene, the expression of which is altered by pathogen infection, a computer-readable medium, a method to confer resistance or tolerance to a plant, a transformed plant, a seed, a method to identify a plant cell infected with a pathogen, a method for marker-assisted breeding comprising said nucleic acid.

Invention 2-3173: claims 1-26, 73-89 partially

same as invention 1 but comprising a gene in the order as given in claim 6 (invention 2 is limited to SEQ ID NO: 2 and invention 3173 is limited to SEQ ID NO: 4737).

Invention 3174: claims 26-77 partially

An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid comprising SEQ ID NO: 2137. A composition, a vector, an expression cassette, a host cell, a plant cell, a transformed plant, a method for augmenting a plant genome, a method to alter the phenotype of a plant cell, a computer-readable medium comprising said polynucleotide.

Invention 3174-5774: claims 26-77 partially

same as invention 3173 but comprising a promoter sequence in the order as given in claim 27 (invention 3174 comprises SEQ ID NO: 2138 and invention 5774 comprises SEQ ID NO: 6813).

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No	
PCT/IB 01/01105	

Patent document cited in search report	Publication date		Patent family member(s)	Publication date
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EP 1033405	A 06-09-2000	CA	2300692 A1	25-08-2000
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